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IGGFDEKURITRRYVDAFNUTJALKYTYAKEKGIR IRMGLSKYRYEKIKKLEBVRKELV
NKTRNKALLOGEIBKOPDDLONIKLRNOTLESSAENVNGIRLPPVLVKTSRKARVEIE
ISDDSKPAHFEFNGAPFTLHDDLSILEGVRRNSIGRAGRATLH"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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BX293986 Mouse DNA
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Gutierrez-Armenta, C.C. and Ramirez-Parra, E.C.
Wheat dp proteins and uses thereof
Patent: WO 0121644-A 1 29-MAR-2001;
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/organism="Triticum monococcum"
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BC015791 Homo sapi
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(c) 1993 - 2005 Compugen Ltd.
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PAT 10-APR-2001

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Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Trache Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticum.

ORGANISM

Ramirez-Parra, E. and Gutierrez, C. Characterization of wheat DP, a heterodimerization partner of th plant E2F transcription factor which stimulates E2F-DNA binding FEBS Lett. 486 (1), 73-78 (2000)

đe

Direct Submission Submitted (03-FEB-2000) Gutierrez C., C.S.I.C.-U.A.M., Centro Biologia Molecular, Cantoblanco, Madrid 28049, SPAIN Location/Qualifiers

2 (bases 1 to 1083) Gutierrez, C.

11108846

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS TITLE

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FEATURES

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ilarity 99.6%;
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PLN 16-DEC-2000

linear

1083 bp mRNA ] protein (dp gene).

TSP271917 1083 bp Triticum sp. mRNA for DP protein ( AJ271917.1 GI:11877790 DP gene; E2F dimerization partner. Triticum sp.

RESULT 2 TSP271917 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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/protein_id="CAC36471.1"
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IRLPFVLVKTSR"
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Triticum monococcum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                              a; Tracheophyta;
Poaceae;
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
Pooideae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                 Gutierrez-Armenta, C.C. and Ramirez-Parra, E.C. Wheat dp proteins and uses thereof Patent: Wo 0121644-A 11 29-MAR-2001; CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.4%; Score 168; DB 6; Lolarity 100.0%; Pred. No. 5.2e-79; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Triticum monococcum"
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| Dax xref="cor:13619661"
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'YRYEKIKKLEEV"
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Triticum monococcum
Eukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae;
Pooldeae, Triticeae, Triticum.
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                                                        539 CAGTITGATGATCTCCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAG
                                                                                                                             ACATTGCATGATGATCTCTCCAATCCTTGAGGGGGTAAGGCGTAACAGCATAGGAAGAGCT
CGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA
                                                                                                            AATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTG
                                                                                                                                                                                                                    659 GAAATTGAGATTTCAGATGACTCGAAGTTTGCCCCATTTCGAGTTCAATGGTGCACCATTC
                                                                                                                                                                                                                                                                                             719 ACATTGCATGATGATCTCTCAATCCTTGAGGGGTAAGGGGTAACAGCATAGGAAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                         CTGGCACAGCCGGATTCTTTGCACAGCTATGTATAGCTATATATCCTCATGAAAACTTG
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                                  CAGTITGATGATCTCCAAAACAICAAGTTACGTAACCAAAACACTGGAAAGCTCAGCAGAG
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Gutierrez-Armenta,C.C. and Ramirez-Parra,E.C.
Mheat dp proteins and uses thereof
Patent: WO 0121644-A 9 29-MAR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
Location/Qualifiers
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15.4%; Score 168; DB 6; I
Best Local Similarity 100.0%; Pred. No. 5.2e-79;
Matches 168; Conservative 0; Mismatches 0;
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Sequence 9 from Patent WO0121644.
AX100712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCTAGTTTATAGGACAGTCT 925
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/protein_id="CAC36468.1"
/db_xref="G1:1361965"
/tanslation="ARAAMAPPRGGAAAATAALDLTGVHILEASSVPPLPERGGNAV
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                                                                                                                               PAT 10-APR-2001
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Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
[ (bases l to 113.)
[ dilaspy, G.E., Keddie, J.S., Oda, K. and Gruissem, W.
Plant inositol monophosphatase is a lithium-sensitive enzyme
                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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Gillaspy,G.E., Keddie,J.S., Oda,K. and Gruissem,W.
Direct Submission
Submitted (20-OCT-1995) Glenda E. Gillaspy, Plant Biology,
University of California, 111 Koshland Hall, Berkeley, CA 94720,
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/organism="Triticum monococcum"
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121 ATAGGAAGAGCTGGCCGCGCCACCCTTCAC 150
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Plant Cell 7 (12), 2175-2185 (1995)
                                                                                                                           AX100708 156 bp
Sequence 5 from Patent WO0121644.
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AX100708
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                                                                                                                           /proteIn_id="CAC36469.1"
/db_xref="G1:13619659"
/ranslation="DKDRKKEKAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADE
1YSBLKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="KARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVRRNSIGRA
GRATLH"
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                                                                                                                                                                                                                                                                                                                                       164 GATAAAGATAGGAAGAAGGAGAAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGC 223
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                    Score 153; DB 6; Length 153;
Pred. No. 6.4e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gutierrez-Armenta, C.C. and Ramirez-Parra, E.C. and wheat dp proteins and usee thereof. Patent: WO 0121644-A 13 29-MAR-2001; CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
                                                                                                                                                                                                                                                                                                0; Indels
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                                                             <1. . > 153
/note="unnamed protein product"
/codon_start=1
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  organism="Triticum monococcum"
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100.0%; Pred. No. c...
0; Mismatches
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                      /mol_type="unassigned DNA'
/db_xref="taxon:4568"
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Sequence 13 from Patent WO0121644.
AX100716
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|db_xref="GI:13619665"
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Triticum monococcum
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Matches 153; Conservative
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Best Local S:
Matches 150
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ORGANISM

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REFERENCE AUTHORS TITLE JOURNAL

REMARK

COMMENT

AUTHORS

JOURNAL MEDLINE PUBMED REFERENCE

TITLE

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Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Eurite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKOZUSE')
Mus musculus chromosome X clone RP23-75B12, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 62 Row: k Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6005885.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 246093)
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Submitted (27-SEP-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR628367.7 GI:52839484
HTG; HTGS PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'translation="VGWEWKVVAAAPQCGEDGAAGGREGAKERRVAE"
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100.0%; Pred. No. 3e-20;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue type="Blood, adult leukocytes"
/clone lib="NIH MGC_118"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Vector: pCMV-SPORT6"
                                                                                                                                                                                    Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="synonym: UNC-18C"
/db_xref="LocusID:6814"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5219755"
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Best Local Similarity
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Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Haich, R.K.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J. Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Buuffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Samallus, D.E.,
Schnerch, A., Schin, J. S., Jones, S. J. and Marra, J., Myers, R.M.,
Schnerch, A., Schin, J. B., Jones, S. J. and Marra, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ברשבעטט
Homo sapiens syntaxin binding protein 3, mRNA (cDNA clone
IMAGE:5219755), partial cds.
                                                                                                                                                                                                                                                                                                                                                       /traislation="MAQNGSVEQFLDVAVEAAKKAGEIIREGFYKTKHVBHKGMVDLV
TETDKACEDFIFNHIKQRFPSHKFIGBETTAACGNFELTDBFFWIVDFLDGTTNFVHG
PRPCVSIGLTIEKKFVGVYVNPIIDELFYGIDGKGAFLNGKPIKVSSGSELVKALL
ATEACTNRDKLVVDATTGRINGLFKKNSLERMGSCALNLCGVACGRLDLFYELEFGG
PWDVAGGAVIVKEAGGFVFDPSGSEFDLTARRVAATNAHLKDAFIKALNE"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1630)
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Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.5%; Score 60; DB 8; Length 1132;
100.0%; Pred. No. 8.8e-21;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                           /product="myo-inositol monophosphatase 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                       location/Qualifiers
                                                                                                                                                                                                                13. ... 819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC028028.1 GI:20380108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1630)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Vector: poTB7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="C110rf10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBMED
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                    shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC002750 444 bp mRNA linear PRI 29-JUN-2004 Homo sapiens chromosome 11 open reading frame 10, mRNA (cDNA clone MGC:3384 IMAGE:3633279), complete cds.
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 28, 2004 this sequence version replaced gi:51966191.
Sequence from the Mouse Genome Sequencing Consortium whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 245993; sum-of-contigs
Insert size: 220507; 3.1% error; agarcse-fp
Quality coverage: 10.26x in Q20 bases; sum-of-contigs Quality
coverage: 12.01x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 2 conties. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the agas are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132816: contig of 132816 bp in length 132916: gap of 100 bp 246093: contig of 113177 bp in length.
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                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 245844 bases at least Q40
Consensus quality: 245914 bases at least Q30
Consensus quality: 245977 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.2%; Score 57; DB 2; Le Best Local Similarity 100.0%; Pred. No. 2.9e-19; Matches 57; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-23"
1. .132816
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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                         COMMENT
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Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.

Straubberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopking, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, K., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Villalon, D.K., Malek, J.A., Gunaratne, E.H., Hulyk, S.W.,
Villalon, D.K., Maley, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,
Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.
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cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (05-FBB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
On Oct 28, 2003 this sequence version replaced gi:12803818.
Contract: MGC help desk
Email: cgapbs-r@mail.nih.gov
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/clone lib="NIH MGC 44"
/lab host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
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Gaps

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Indels

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INV 16-JUN-2002

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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular CDNA clone. However, there artifacts associated with the generation of CDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDDKSKKELLRNKSNPVVSRAAANCAVNMFRTKVAENAKNQDDKHIKQNGDILIDPDD
DEQIESLLKEALRVLRGNRQYVLATLSNAHKMPVLLDWVADRYGKSYCRAGMKSIVKT
SFRIYEKVYEKERRNKRNMLELKRSVTGLGSSISYASHKKFMSQVVQRKAEYNNKLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1985)
Stableton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MLDVVGDELKARRKHILNDIENNVKWASNRMKRQLGITSGPVKL
AKASRTARKKKKEPNILIGLGNGEENPRLHSYAHSLNNSIRVMLMKGNESHRCGAGDCEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDVDCEMKGSAEITMKPQNVKSFIEEKPRLPTSSFKKLADLIPVCSRTLRSLKRSSPK
APAEESFTINRSIGGFQLDYHKIFDVPLPLVEPMPWEDEVMDLEDKQPVIERFCIDALG
                                                                                                Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
                                                                                                                                                                                                                                                                   AY118692 1985 bp mRNA linear
Drosophila melanogaster AT17414 full insert CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      FLI_CDNA.
Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_id="AAM50552.1"
db_xref="GI:21429748"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cdna@fruitfly.berkeley.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Longest ORF"
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                                                                                                                                                                                                                                                                                                                                                        AY118692.1 GI:21429747
                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
         56; Conservative
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                                                                                                                  /trānslation="MELEAMSRYTSPVNPAVFPHLTVVLLAIGMFFTAWFFVYEVTST
KYTRDIYKELLISLVASLFMGFGVLFLLLWVGIYV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRI 11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susama Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice Mcheavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Dunne Smailus, Michael Smith, Lorraine Spence, Jeff Stott. Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1980)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: j Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
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'product="chromosome 11 open reading frame 10"
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                                                                                                                                                                                                                                        Length 444;
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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/clone lib="NIH MGC 15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                   1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1980 bp mRNA
Homo sapiens, clone IMAGE:4866083, mRNA.
BC015791
                                                                                                                                                                                                                                     Score 56; DB 9;
Pred. No. 1.3e-1
                                                                                                                                                                                                                5.1%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
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/db_xref="GI:12803819"
/db_xref="T.com.rr"
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1. 1980
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC015791.1 GI:16041805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                               56; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                Local Similarity
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ORGANISM

REFERENCE AUTHORS JOURNAL

REMARK COMMENT

FEATURES

ORIGIN

RESULT 12 BC015791

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Matches

LALEQSRLTWLALRGYSHLGGSIKDTFFAYMPARPQDIKROHIWKSYOFLDMVNFRLR

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Vector:
Vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 2084)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submission
Submission
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashimih-go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111 (ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolation of novel full-length cDNA clones from macaque testis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLMLMLVAAVTMMLRPLVTAQPLCRARTVRTGKVFNVIQDVQGD
RLYFRSTTTRLIKHPCKKNIALYLGKQVFFTTDNFETSLLPFTIPSSMQVGVPEVTSA
HFTGSLLLLVVNHKVYTYDYESNSWNLSLGIKHPVTHVSGDNCCYTGSLFCVDVSNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osada, N., Hida, M., Kusuda, J., Tanuma, R., Hirai, M.,
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/clone_lib="macaque_testis_cDNA_library_QtsA"
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                                                                                                                 Length 1985;
                                                                                                                                                                                       0; Indels
                                                                                                         5.1%; Score 56; DB 3; Le
100.0%; Pred. No. 1.2e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABÖ72761
BO72761.1 GI:16041125
Oligo capping; fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.K., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.K., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Youchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A. FAYFRGDQISQTYIYYSNTGGFSFWKYHYDRQAEIVGSLGGIFHLFSLSQVGMLVVDQ GKGMFKYSDHPLNRSLGLSFDYNGTLDIVIATFYESGYTSDGNTKYKLDIYLKQQQHW GRTDFNFTSSLKRATMSTLTVDIANKEISCVDIKPLSTLISVGCDLDKKIVIENTVSA CSKGVLDALALQDNYSFIIEKEFYDPGFQGRQSSKDLHVFYSYQQLGCPLLVYYDTPW KPVVELWKKDRFQEVVDAEYVLLEVNGQFSYSYSLTAKSAMCTSQPQNWTTMIKESGG PFWNRENYSCHDPNNDAPLRANDVQYQLLGGRTANQIVFSHNNGFYVFYISIVDPY YSYCQLETVESIYVYGAFPVQLVSAGVVMVLLISSILGSVWLAYMIPRLLRTARGRRM TSFVAQLYGRCKTVCQFRASATASKPMGRHRSS" ö BC065220 3430 bp mRNA linear PRI 03-FEB-2004 Homo sapiens KIAA0602 protein, mRNA (cDNA clone IMAGE:5732786), partial cds. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3430) Submitted (12-JAN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Contact: nisc\_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) ö 5.1%; Score 56; DB 9; Length 2084; 100.0%; Pred. No. 1.2e-18; Live 0; Mismatches 0; Indels NIH-MGC Project URL: http://mgc.nci.nih.gov Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/ Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Invitrogen BC065220.1 GI:40850907 Homo sapiens (human) (bases 1 to 3430) 56; Conservative Direct Submission Strausberg, R. Homo sapiens Best Local Similarity BC065220 12477932 Query Match Matches DEFINITION ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 15 ACCESSION VERSION KEYWORDS JOURNAL REFERENCE AUTHORS REMARK COMMENT BC065220 ORIGIN SOURCE LOCUS ð 셤

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 139 Row: i Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
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KARTILGYKTLAAGSISMAEVWQHSEBGGGVETDLATFSLQYPFLKREGKKLQIMLQRRKRY
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SIVRTSSMTRQQYFKQKVVALLRFKYSBEYLDSEQDPABHTPEAEBLDLLIJTJTLDH
EHPSDSGPBWEDDDSVLSTPRKPKLPFYYSBEGLSSSQTEIGSISBRSBHKEPPSPADV
PEKTRSLGGRQPSDSVSDTYALGVFPREHPGQPEDSPARAASTLDVFTERLPPSGFI
YKTESLVIPSTRSBERQAGRRRRSTSLKERQAARPQNERANSLDNBKCPDARSQLQIP
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VIRTESLVIPSTRSBEGVDYRKRRSTSLKERQAARPQNERANSLDNBKCPDARSQLQIP
STIVRSLQYRYGVSVQPTVVKIAVAGAQHTLASTLIALFVYCTCSPADVQAA
VIPLGSHPVARYLGSVDYRYNNFFQDLAMRDLFWKLEAQLSVQTVTAG
VIPLGSHPVARYLGSVDYRYNNFFQDLAMRDLFWKLEAQSAVQDTPDIVSRITQYIAG
ANCAHQLPIABAMLIYKQKSPDEESSQKFIPPVGVVKVGIVEPSSATSGDSDDAAPSG
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RIGLPGAAPGALNTPVPWNLFATWEVDGSSPSCVPRLCSLTLKKLVVFKELEKELISVV
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RKRDAEKKDLPVTKNTLKCTPRSLQVSRLPSSGEAAATPTMSMTVVTKEKNKKVMFLP
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HFPICIFGHSKATF"
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, K., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="Brain, hippocampus"
/clone_lib="NIH MGC_124"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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<1. .3430
/gene="KIAA0602"
/db xref="LocusID:23241"
//db xref="LocusID:23241"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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; 0 Query Match 5.1%; Score 56; DB 9; Length 3430; Best Local Similarity 100.0%; Pred. No. 1.2e-18; Matches 56; Conservative 0; Mismatches 0; Indels

ઠે 셤 Search completed: February 6, 2005, 20:16:32 Job time : 5152 secs

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TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-13903
RESULT 1
US-09-311-021-191
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8656, Ap
Sequence 8127, Ap
Sequence 801, App
Sequence 10675, A
Sequence 19144, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25, Appl
27, Appl
27, Appl
16, Appl
16, Appl
463, Appl
31, Appl
73, Appl
37, Appl
37, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 191, App
Sequence 13903, A
                                                                               (without alignments)
7884.537 Million cell updates/sec
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                                                                                                                                 Description
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                                                                    February 6, 2005, 15:46:16; Search time 226 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-621-976-13903

US-09-185-1418-1

US-09-322-409-25

US-09-451-527-25

US-09-451-527-25

US-09-451-527-25

US-09-482-273-58

US-09-800-729-73

US-09-800-729-73

US-09-800-729-73

US-09-800-729-73

US-09-800-729-73

US-09-800-729-73

US-09-800-729-73

US-09-801-976-8656

US-09-621-976-86127

US-09-621-976-86127
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                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
                                               - nucleic search, using sw model
                                                                                                                                                   OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                    Issued Patents NA:*
                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                            US-10-088-830-1
1089
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Match Length
                  . Copyright
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                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                        Word size :
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                                                                    Run on:
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No.
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                               Sequence 1, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 110, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 110, Appl
Sequence 110, Appl
Sequence 110, Appl
                                                                                                                                                                                                                                                   Sequence 6, Appl
Sequence 6, Appl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Genetics Institute, Inc.
APPLICANT: Agostino, Michael J.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SEREETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6300-11A
CURRENT FAPLICATION NUMBER: US/09/311,021
CURRENT FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 268
SOFTWARE PATENCE.
SEQ ID NO 191
LENGTH: 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dumas Mine Edwards, J.B.
APPLICANT: Johnert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054 PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 13003
LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Le
1.2e-13;
                                                            US-09-205-258-186
US-09-101A-4
US-09-149-476-310
US-09-108-065-040-2
US-09-108-476-186
US-08-960-022-17
US-09-688-096-11
US-09-688-096-11
US-09-668-096-11
US-09-668-096-11
                                                                                                                                                                                                                                US-10-115-123-110
US-08-300-903A-6
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100.0%; Pred. No. 1.-...
0; Mismatches
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US-10-385-072-6
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; Sequence 13903, Application US/09621976
; Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 191, Application US/09311021 Patent No. 6706869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 55; Conservative
TYPE: DNA
GRGANISM: Homo sapiens
US-09-311-021-191
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CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
RUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 27, Application US/09322409
; Patent No. 6471957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA; Canis familiaris US-09-322-409-27
                                                                                                                                                                            TYPE: DNA ORGANISM: Canis familiaris
                                                                                                                                                                                                                                    , NAME/KEY: CDS
; LOCATION: (74)..(901)
US-09-322-409-25
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Batent No. 6411957

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee

APPLICANT: Vang, Shumin

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC TITLE OF INVENTION: CANINE AND USES THEREOF

FILE REFERENCE: IM-2-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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100.0%; Pred. No. 3e-13;
tive 0; Mismatches 0; Indels
                                Length 176;
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Zhang, Lei
APPLICANT: Yujay, Hari M.
APPLICANT: Node, Harid M.
APPLICANT: Rode, Harold
TITLE OF INVENTION: ALLERGEN OF CLADOSPORIUM HERBARUM
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby and Maclean
SIREET: 880 Wellington Street, Suite 708
                                5.0%; Score 54; DB 4; Le Best Local Similarity 100.0%; Pred. No. 3.4e-13; Matches 54; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA and its encoded protein FEATURE: open reading frame of CH2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Octawa
COUNTRY: Canada
COUNTRY: Canada
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TRY-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,414E
FILING DATE: January 24, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REFERENCE/DOCKET NUMBER: 1747
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: NUCleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              Sequence 1, Application US/08185414E Patent No. 5556953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 54; Conservative
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US-08-185-414E-1
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Sequence 25, Application US/09451527

Fatent No. 6482403

GENERAL INFORMATION:

APPLICANT: Yang, Shumin

APPLICANT: Yang, Shumin

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-2-C2

CURRENT APPLICATION NUMBER: US/09/451,527

CURRENT APPLICATION NUMBER: 09/322,409

EARLIER PILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Wonderling, Shumin S.
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REPERRICE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
EARLIER APPLICATION NUMBER: US/09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER FILING DATE: 1998-05-29
NUMBER FOR SEQ ID NOS: 15-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 985;
Length 985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.0%; Score 54; DB 4; Le
100.0%; Pred. No. 2.9e-13;
tive 0; Mismatches 0;
Score 54; DB 4; Le
Pred. No. 2.9e-13;
      Query Match 5.0%; Score 54; DB Best Local Similarity 100.0%; Pred. No. 2.9 Matches 54; Conservative 0; Mismatches
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Length 1023;
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                          ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,966B
FILING DATE: 01-010-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.0%; Score 54; DB 1; L
100.0%; Pred. No. 2.9e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.0%; Score 54; DB 4; Loudo.0%; Pred. No. 2.9e-13; live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al. TITLE OF INVENTION: 71 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT PILING DATE: 2000-01-13
EARLIER PEPLICATION NUMBER: PCT/US99/15849
EARLIER PELING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER PELING DATE: 1999-07-14
EARLIER PELING DATE: 1998-07-15
EARLIER PELING DATE: 1988-07-15
EARLIER PELING DATE: 1988-07-15
EARLIER PELING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
                                                                                                                                                                                                                                                       MAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997.
REFERENCE/DOCKET NUMBER: PHCR17694
TELECHOMNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELERAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGRITH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: clone 20; see Figure 27
HYPOTHETICAL: NO
ORIGINAL CAPACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 58, Application US/09482273
Patent No. 6534631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58
LENGTH: 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.0
Best Local Similarity 100.
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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CORGANISM: Homo sapiens
US-09-482-273-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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FREELING TINFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Watchew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: Im-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT APPLICATION NUMBER: 09/322,409
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER PILING DATE: 1990-05-28
EARLIER PILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 985
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson, and KindnessPLLC STREET: 1420 Fifth Ave., Suite 2800 CITY: Seat1e STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Elsenman, Robert N.
APPLICANT: Hurlin, Peter J.
APPLICANT: Ayer, Donald E.
APPLICANT: Ayer, Bonald E.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
TITLE OF INVENTION: Mad or Max
                                                                                                                                                                                                                                                                                                       5.0%; Score 54; DB 4; Length 985;
100.0%; Pred. No. 2.9e-13;
Live 0; Mismatches 0; Indels
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EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08252966B Patent No. 5624818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27, Application US/09451527 Patent No. 6482403
                                                                                                                                            TYPE: DNA ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100. Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Canis familiaris
                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (74)..(901)
US-09-451-527-25
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US-09-451-527-27/c
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Sequence 77, Application US/09800729

Sequence 77, Application US/09800729

PATENT NO. 605592

TILLS OF INVENTION:

TILLS OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/800,729

CURRENT PAPLICATION NUMBER: POT/US00/26013

PRIOR FILING DATE: 2001-03-08

PRIOR PPLICATION NUMBER: 60/155,709

PRIOR APPLICATION NUMBER: 60/155,709

PRIOR APPLICATION NUMBER: 60/155,709

PRIOR APPLICATION NUMBER: 1999-09-24

NUMBER OF SEQ ID NOS: 217

SEQ ID NOS: 217

SEQ ID NO 77

LENGTH: 1811
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GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZ044P1
                                                                                              CURRENT APPLICATION NUMBER: US/09/800,729; CURRENT FILING DATE: 2001-03-08; PRIOR APPLICATION NUMBER: PCT/US00/26013; PRIOR FILING DATE: 2000-09-24; PRIOR APPLICATION NUMBER: 60/155,709; PRIOR FILING DATE: 1999-09-24; NUMBER OF SEQ ID NOS: 217; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 73; LENGTH: 1810
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:

NAME/KEY: SITE

LOCATION: (1803)

CTHER INFORMATION: n equals a,t,g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-77
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Patent No. 6512164
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (1804)
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US-09-594-506-37
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                                                                                                                                           APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 05/09/949,016
RIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-09
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APPLICANT: Mahajan, Pramod B.
TITLE OF INVENTION: A No. 6720478el Maize Rad51-Like Gene and Uses
TITLE OF INVENTION: Thereof
FILE REPERENCE: 1107
CURRENT APPLICATION NUMBER: US/09/537,654
CURRENT APPLICATION NUMBER: 60/132,582
EARLIER APPLICATION NUMBER: 60/132,582
EARLIER FILING DATE: 1999-05-05
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1459
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100.0%; Pred. No. 2.8e-13;
tive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 463
LENGTH: 1358
                                                                        Sequence 463, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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Matches 54; Conservative
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) LOCATION: (169)...(1011)
US-09-537-654-3
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US-09-949-016-463
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US-09-800-729-73
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US-09-537-654-3

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TYPE: DNA

Query Match

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TYPE: DNA

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; Sequence 73, Application US/09800729

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Fatent No. 6657054
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Requilated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT PAPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LIGHTH: 3438
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APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Thiamine Biosynthetic Enzymes
FILE REPERENCE: BB1372 US NA
CURRENT APPLICATION NUMBER: US/09/594,506
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/139,556
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Microsoft Office 97
LENGTH: 2406
                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-594-506-37
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; NAME/KEY: CDS
; LOCATION: (527)..(2701)
; OTHER INFORMATION:
US-10-164-595-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-10-164-595-29
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Search completed: February 6, 2005, 17:39:37 Job time: 228 secs

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601492711 99AS179 R

201003.pl Mdfr3002d 99AS164 R

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Title: Perfect score:

Sequence:

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Scoring table:

Word size :

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Database :

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Triticum aestivum (bread wheat)

IsM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldaes: Triticaee; Triticaee; Triticaee; Triticae.

1 (bases | Triticaee; Triticam.

2 Lamoureux, D., Peterson, D.G., Li, W., Fellers, J.P. and Gill, B.S.

2 Lamoureux, D., Peterson, D.G., Li, W., Fellers, J.P. and Gill, B.S.

3 Lamoureux, D., Peterson, D.G., Li, W., Fellers, J.P. and Gill, B.S.

4 Cot-based cloning and sequencing (CBCS) efficiently removes equencing (CBCS) efficiently removes equencing (2004)

5 Cot-based cloning and sequencing (CBCS) efficiently removes equencing the part pathology (Ansas State University Ansas State University 1911

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 CCGCAATGGCCCCCCCCCGCGGGGCTGCTGCGGCCGCTACCGCCGCACCTGA 608
                       B1377034 BFLG3
CD722238 GJ07b1
BG164238 GJ07b1
CK938853 CGF100
B1377687 BFLG3
CD92266 C92006 D
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CN992267 70294
BISC1964 G03391
BUSS035 AGENCO
BE97803 GACO
BE97803 GACO
BE229946 99AS17
AM481765 37984
CK121861 HD--07
AM481765 37984
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CK121863 BE22991
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| /organism="Triticum aestivum" |
| /mol_type="genomic DNA" |
| /mol_type="connic DNA" |
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| /clone="1188HCOIN01" |
| /tissue_type="whole plant" |
| /dev_stage="young shoot" |
| /clone_lib="1188HC library"
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                                                               CK938853
BI377687
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Location/Qualifiers
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tes 107; Conserv
 Query Match
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VERSION...
KEYWORDS
SOURCE
ORGANISM
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CL902823
LOCUS
DEFINITION
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Matches
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AUTHORS
TITLE
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                                                                                    6, 2005, 17:09:27 ; Search time 4251 Seconds (without alignments) 9751.115 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                            nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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gb_est2:*
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CA802821
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                                                                                                              CD892664 454 bp mRNA linear EST 14-JUL-2003 GI18.121J723F010725 GI18 Triticum aestivum cDNA clone GI18121J73, mRNA sequence.
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Triticum aestivum
Triticum aestivum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                         93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fishs sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                         Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="recital"
/cultivar="recital"
/clone="G118121J23"
/tissue type="grain (118 degrees per day after
pollination"
 Query Match 9.0%; Score 98; DB 6; Length 454; Best Local Similarity 99.3%; Pred. No. 5.9e-36; Matches 148; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Triticum aestivum"
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CD882927.1 GI:32645392
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CD882927
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1 (bases 1 to 301)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Bock, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
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When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Putative full length read vector to vector length is 467 Seq primer: -40RP from Gibco
High quality sequence stopp: 286.
Location/Qualifiers
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Tel: 33 1 69 47 54 00

Tel: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (http://www.genoplante.com

and http://genoplante-info.infobiogen.fr).
Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 649;
4e-31;
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                                                                                                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
/mol type="mskN"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="FtllILL02"
/tissue_type="leaf one"
/clone_lib="Ft"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%; Score 88; DB
100.0%; Pred. No. 4e-
live 0; Mismatches
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Best Local Similarity 100.
Matches 88; Conservative
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/clone_lib="Gm-c1071"
/clone_lib="Gm-c1071"
/clone_lib="Gm-c1071"
/clone_lib="Gm-c1071"
/clone_lib="Gm-c1071"
/clone_lib="Gm-c1071"
/clone_lib="Gm-c1071"
/clone_lib="Gm-c1071"
/clonelibe yes constructed_from mRNA isolated from immature pods (approximately 2cm long) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restrictions site. Sall linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-Sall restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into a cools ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinios at Urbana-Champaign. email: l-vodkin@uiuc.edu"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosida I, Malpighiales, Salicaceae, Saliceae, Populus.
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/clone="SOYBEAN CLONE ID: Gm-c1071-3748"
/tissue_type="immature pods (~2cm long) of greenhouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Teichmann, T.,
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Brosche, M., Alatalo, E.R., Vinocur, B., Altman, A., Teichmann, T.
Ottow, E.A., Polle, A., Djilanov, D., Afif, D., Triboulot, M.B.,
Greyer, E., Paulin, L. and Kangasjaervi, J.
Gene expression in desert leaves
Unpublished (2004)
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/note="country: China:Xinjiang"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.4%; Score 59; DB 6; Length 301;
100.0%; Pred. No. 4.4e-17;
live 0; Mismatches 0; Indels
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Department of Biosciences, Plant Physiology
University of Helsinki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Populus euphratica"
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/db_xref="taxon:75702"
/clone="P0000300024G01F1"
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                         /organism="Glycine max"
                                               /mol_type="mRNA"
/cultivar="Williams"
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Location/Qualifiers
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AJ774826.1 GI:50066501
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Score 59; DB 1; Length 318; Pred. No. 4.4e-17;

5.4%; S 100.0%;

Query Match Best Local Similarity

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/clone="Targerary graphs of the cells" / dev_stage="3 day" | /dev_stage="3 day invitro bradyzoite" | /clone lib="TagME49 3 day invitro bradyzoite" | /clone lib="TagME49 3 day invitro bradyzoite" | /note="vector: paluescript SK; Site= 1: Not!; Site=2: Smal; CDNA was reverse transcribed using Superscript II and an anchored (?wobble') oligo dt primer, containing a NOTI restriction strand cDNA was digested with NOTI restriction endonuclease, purified and size fractionated with a SizeSep 400 spun column (Ameraham) and directionally cloned into the Smal and NotI sites of phluescript SK. Pollowing electroporation into ElectronTen Blue cells (Stratagene), 5 x 106 primary CFU were bottle amplified in semisolid culture media [2xLB+15% SeaPrep agarosed (BWA)]. After 48 hrs at 30 degrees Celcius, cells were harvested, pooled and stored in 2xLB + 15% glycerol ."
                                                                                                                                                                                          LD3/1210
TGESTZYG99C09.x1 TGME49 3 day invitro bradyzoite Toxoplasma gondii
CDNA clone TGESTZYG99C09.x1 3', mRNA sequence.
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Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Putative full length read
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1 (bases 1 to 157)
Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Matin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Kitter, E., Bennett, J., Franklin, C., Tasgareishvill, R., Ronko, I., Konnedy, S., Magnire, L., Waterston, R. and Wilson, R.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TTE1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
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Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 58; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector to vector length is
Seg primer: -40UP from Gibco.
Location/Qualifiers
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Contact: Clifton,
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CO249876.1 GI:49121395
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CO249876
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                  AL697897 1686 (synonym: hlcc3) Homo sapiens CDNA clone DKFZp686A19105 1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 169)

Koehrer, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S. EST (Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 177)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="DKFZp686A19105"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                                                                                                                                                                                                              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2); Email 3. Wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone (DKFZp686A19105) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.1%; Score 56; DB 1; Length 169; Best Local Similarity 100.0%; Pred. No. 1.3e-15; Matches 56; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No s1 sequence available.
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SM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 214)

SNIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Mary Hendrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="adenocarcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/loote="Organ: prostate; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Site_1: Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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//mol_type="mRNA"
//db xref="texon:9606"
//clone="INAGE:3092506"
//tissue_type="Chondrosarcoma Lung Metastasis cell lines"
//tissue_type="Chondrosarcoma Lung Metastasis cell lines"
//tissue_type="Chondrosarcoma Lung metastasis
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//note="Organ: Lung; Vector: pXX-Asc; Site l: EcoR I;
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//clone lih="Organ: Lung; Vector: pXX-Asc; Site l: EcoR I;
//clone lih="Organ: Lung; Vector: pXX-Asc; Site lihe"
//clone lihe"
//cl
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Phttp://image.llnl.gov
Plate: NDAM1168 row: i column: 12
High quality sequence stop: 214.
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10188 row: g column: 10
High quality sequence start: 3
High quality sequence stop: 169.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4432161"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
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DRIGIN

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Washington University School of Medicine
4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 2800
Fax
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/db xref="rational"
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grown plants"
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cDNA library was constructed from mRNA isolated from
immature pods (approximately 2cm long) of greenhouse grown
plants. The library was prepared using the Life
Technologies pSuperScript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a
poly(dT) sequence with a Not1 restrictions site. Sal1
gel. First strand cDNA synthesis was primed with oligo-dT primer containing a NoI I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into PXY-Asc vector. The library tag sequence located between the Not I site and the polya is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 7; Le
Pred. No. 1.3e-15;
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TITLE COMMENT FEATURES

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linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Uvokxin by Anu Khanna at the University of Illinios at Urbana-Champaign. email: l-vodkin@uluc.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Brain; Vector: pBluescript II SK; Site_1: EcoRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. wark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street,
                                                                                                                                                                                                                                                                 ö
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CN005830 262 bp mRNA linear EST 26-MAR-2C ip35e06.gl Brain - Cerebellum Library (DOGEST8) Canis familiaria
                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                       Length 223;
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/dev_stage="3 month old normal canine"
/lab_host="XLI0 Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2004)
Contact: W. Richard McCombie
Contact: W. Richard McCombie
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Par: 516 367 884
Pax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 262)
Balija,V., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris cerebellum (dog)
                                                                                                                                                                                                                       DB 6; Le
1.3e-15;
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/organism="Canis familiaris"
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                                                                                                                                                                                                                     5.1%; Score 56; DB
ilarity 100.0%; Pred. No. 1.3
Conservative 0; Mismatches
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/db_xref="taxon:9615"
/clone="ip35e06"
/sex="Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mccombie@cshl.org
Plate: ip35 row: e column: 06
High quality sequence stop: 276.
Location/Qualiflers
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VERSION

RESULT 12 AW734913

ORGANISM

KEYWORDS SOURCE

AUTHORS REFERENCE

TITLE JOURNAL

COMMENT

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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkf2- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
AL046990

DKFZD586L2017_r1 586 (synonym: hutel) Homo sapiens cDNA clone
DKFZD586L2017_5', mRNA sequence.
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603030013F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5200226 5',
mRNA sequence.
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Homo sapiens
Homo sapiens
Bukaryota; Metaca; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 290)
                                                                                                                                                                                                                                                                                                                                                                     Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone (DKFZp58612017) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S. EST (Kochter, et al.)
Unpublished (1999)
On Jul 9, 1999 this sequence version replaced gi:5435046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 287;
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100.0%; Pred. No. 1.3e-15;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp586L2017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="uterus"
|dev_stage="adult"
|lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 287)
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BI756116.1 GI:15747694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Email: estewatson wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTS on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Seq primer: -40RP from Gibco
High quality sequence stop: 227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The series of th
                                                                                     269 bp mRNA linear EST 14-JUL-2004 GM-011.yl Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: GM-c1016-10054 5', mRNA sequence.
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Glycine max
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FEATURES

RESULT 13 AL046990

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Indels

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/lab.host="NHIOB"
/clone lib="NHH MGC 114"
/note="Organ: brain; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGESTO036 Anopheles gambiae adult pSport cDNA Anopheles gambiae Adult pSport cDNA Anopheles gambiae AA413331
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/clone lib="Anopheles gambiae adult pSport cDNA"
/note="Site 1: Sal1; Site 2: Not1; See: Salazar, C.E.,
al. Insect Molecular Biology (1994), 3:1-13."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles gambiae
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cornel, A.J., Kumar, V., Mukabayire, O., Salazar Rafferty, C., Petrarca, V., Coluzzi, M. and Collins, F.H.
A comprehensive physical map of the malaria vector Anopheles
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11501 row: j column: 03
High quality sequence stop: 236.
Location/Qualifiers
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Other_ESTs: AgEST00035
Contact: Salazar Rafferty, C.; and Collins, FH
Vector Genetics Section
Centers for Disease Control and Prevention
MS F-22, 4770 Buford Hwy, Chamblee, GA 30341
Fax: 770 488 7469
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Mapping location: 34C in 3R chromosome
Seq primer: M13 Universal
High quality sequence stop: 294.
Location/Qualifiers
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                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5200226"
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/clone="cc38"
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1 (bases 1 to 294)
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OM nucleic - nucleic search, using sw model

February 6, 2005, 14:35:16; Search time 698 Seconds (without alignments) 9235.814 Million cell updates/sec Run on:

US-10-088-830-1 1089 Title: Perfect score:

Sequence:

OLIGO NUC Gapop 60.0 , Gapext 60.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters: 0 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

N\_Geneseq\_16Dec04:\*
1: geneseqn1980s:\*
2: geneseqn1990s:\*
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9: geneseqn203as:\*
9: geneseqn203as:\* geneseqn2004as:\* geneseqn2004bs:\* geneseqn2003cs:\* geneseqn2003ds:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		* Ouery					
No.	Score	Match	Match Length DB	80	ΩI	Description	
1	965	98.6	1089	4	AAF80144	Aaf80144 Nucleotid	
7	168	15.4	168	4	AAF80149	Aaf80149 DNA fragm	
m	168	15.4	168	4	AAF80148	Aaf80148 DNA fragm	
4	153	14.0	153	4	AAF80147	DNA	
S	150	13.8	150	4	AAF80150	DNA	
9	114	10.5	156	4	AAF80146		
7	26	5.1	668	Ŋ	AAH64916	Aah64916 Human sec	
80	55	5.1	376	ß	ABV58410	Abv58410 Human pro	
6	52	5.1	396	m	AAD02077	Aad02077 cDNA enco	
c 10	52	5.1	410	æ	ABX42327	Abx42327 Bovine ES	
11	55	5.1	443	4	AA190926	Aai90926 Human pol	
12	52	5.1	491	m	AAZ52570	Aaz52570 Human sec	
13	55	5.1	917	m	AAC77635		
14	55	5.1	2435	12	ADQ22529	Adq22529 Human sof	
15	55	5.1	3759	е	AAC58600	Aac58600 Human PRO	
16	55	5.1	3819	~	AAZ34292	Aaz34292 Human PRO	•
17	55	5.1	3819	m	AAC78580	Aac78580 Human PRO	
18	55	5.1	3819	4	AAS21446	Aas21446 Human cDN	
19	55	5.1	3819	9	ABK33602	Abk33602 cDNA enco	
20	55	5.1	3819	9	ABL88117	Ab188117 Human PRO	

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ABL9560 ACA72020 ACA72020 ACA72020 ACA72020 ACA6640 ACA6856 AC	ADB30585 ADA85881 ADA97093 ADA79397
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	4 4 4 4 9 6 4 7

## ALIGNMENTS

E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation; Nucleotide sequence of a wheat E2F-dimerisation partner (DP) protein. AAF80144 standard; DNA; 1089 BP. 11-JUN-2001 (first entry) AAF80144; 

Location/Qualifiers 20. .805 /\*tag= a /product= "B2F-dimerisation partner (DP) protein" Triticum monococcum.

WO200121644-A2.

29-MAR-2001.

25-SEP-2000; 2000WO-EP009325.

99ES-00002127. 24-SEP-1999; 11-NOV-1999; (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.

Gutierrez-Armenta C, Ramirez-Parra E;

WPI; 2001-257972/26. P-PSDB; AAB67762.

New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.

Claim 13; Fig 1; 77pp; English.

The present sequence encodes a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to Sphase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F-DP domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue size 8 $\pm$ 8

Sequence 1089 BP; 367 A; 215 C; 261 G; 246 T; 0 U; 0 Other;

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244 184 244 304 364 484 484 544 664 724 665 GAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTCAATGGTGCACCATTC 724 784 844 844 904 304 364 424 544 CAGITIGAIGAICICCAAAACAICAAGITACGIAACCAAACACIGGAAAGCICCAGCAGAG 604 604 664 784 904 ACCTAGITITATAGGACAGICICICAGGCTIGAGAAGAITITIAACCIGCAAAITITIGICIC 964 964 GAGCTGAAGTCCATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGA CTGGCACAGCCGGATTCTTTTGCACAGCTATGTATAGCTATATATCCTCATGAAAACTTG ACCTAGTITATAGGACAGTCTCTCAGGCTTGAGAAGATTTTAACCTGCAAATTTTGTCTC GCCGGTAATGCGGTCCAAAGGAAGGGGCCTGTTGACCCGGATAAAGATAGGAAGAAGAAGAG GGCGGTAATGCGGTCCAAAGGAGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGAG GAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCA GAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCA ATACGGTGGATGGGCCTTTCAAATTACAGATATGAAAAAATAAAGAAGCTTGAGGAAGTT CGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA AATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTG ACATTGCATGATGTCTCTCAATCCTTGAGGGGGTAAGGCGTAACAGCATAGGAAGAGCT GGCCGCCCCCCCTCACTAGAGACTCAAGAATATTACAAATGAATTAAAAGTGTTAGAA GGCCGCCCCCCTCACTAGAGCTCAAGAATATTACAAATGAATTAAAAGTGTTAGAA CTGGCACAGCCGGATTCTTTTGCACAGCTATGTATAGCTATATATCCTCATGAAAACTTG AAGGCTGCGGCACCAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATGTTTGT CAGTITIGATGATCTCCAAAACATCAAGTTACGTAACCAAAACACTGGAAAGCTCAGCAGAG AATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTG GAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTCAATGGTGCACCATTC AAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGT GAGCTGAAGTCCATGCCACATATTGGTCAAGGGTTTTGATGAGAAGAATATTAGGCGGAGA ACATTGCATGATGATCTCTCAATCCTTGAGGGGGTAAGGCGTAACAGATAGGAAGAGCT Gaps ö DB 4; Length 1089; 0; Indels Query Match 88.6%; Score 965; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 965; Conservative 0; Mismatches 185 245 545 545 605 725 485 125 125 185 245 305 305 365 365 425 425 485 605 665 725 785 785 845 845 905

AAF80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase profression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to superss certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, ö phase; New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size. 2P-dimerisation partner; DP protein; E2F transcription factor; G1 pha phase; cell cycle; retinoblastoma protein; alter cell proliferation; 965 CTTTTTGTGCCTAGCAGGTTATTAGGTCTCAGATAGATGATTCATATATGTGCTGCTATG 485 CGTAAAGAACTCGTCAACAATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA DNA fragment encoding a wheat E2F-dimerisation partner (DP) protein Length 168; Indels Sequence 168 BP; 62 A; 38 C; 33 G; 35 T; 0 U; 0 Other; 15.4%; Score 168; DB 4; Lularity 100.0%; Pred. No. 1.8e-49; Conservative 0; Mismatches 0; (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF. Ä Disclosure; Page 74-75; 77pp; English. Ramirez-Parra ВР 99ES-00002127. 25-SEP-2000; 2000WO-EP009325 AAF80149 standard; DNA; 168 (first entry) Gutierrez-Armenta C, organ or tissue size WPI; 2001-257972/26. P-PSDB; AAB67767. Triticum monococcum 1085 AAAAA 1089 AAAAA 1089 Best Local Similarity Matches 168; Conserv E2F-dimerisation WO200121644-A2 24-SEP-1999; 11-NOV-1999; 11-JUN-2001 29-MAR-2001 1025 965 AAF80149; Query Match RESULT 2 AAF80149 셤 g g ઠે ò ò

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AAF80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription actor. Eactor. E2F and DD are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell progression. E2F and retinoblatement protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly organ or tissue size.
                                  604
                                                                  61 CAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAG 120
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1 CGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA 60
                                  CAGITICATGATGATCTCCAAAACATCAAGTTACGTAACCAAAACACTGGAAAGCTCAGCAGAG
                                                                                                                                                                                                                                                                                                                            DNA fragment encoding a wheat E2F-dimerisation partner (DP) protein.
                                                                                                    652
                                                                                                                    121 AATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGG 168
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                                                                                                 605 AATGTTAATGGCATCCGCTTCCATTCGTATTGGTCAAGACATCTAGG
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AAF80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a heterodimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue size
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                                                                                   121 GGCCTTTCAAATTACAGATATGAAAAATAAAGAAGCTTGAGGAAGTT 168
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al Similarity 100.0%; Pred. No. 3.4e-44;
153; Conservative 0; Mismatches 0;
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DNA fragment encoding a wheat E2F-dimerisation partner
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                                 RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DNA fragments of a a plant E2F transcription factor. E2F and DNA fractor. E3F and DNA fractor transcription factor that regulates G1 to S phase of the call cycle, and later, the expression of genes required for S-phase progression. E2F and retlinoblastoma protein also interact as a heterodimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell,
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                                                                                                                                                                                                                                                                                                                                      E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAAGCAAGGTGGAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTCAAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.
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                                                                                                                                                                                                                                                                                             DNA fragment encoding a wheat E2F-dimerisation partner (DP) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
13.8%; Score 150; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.8e-43;
Matches 150; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF
                     121 GTTGCAGACGAAATTTATTCAGAGCTGAAGTCC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAGGAAGAGCTGGCCGCCCCCTTCAC 802
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                                                                                                                                                             AAF80150 standard; DNA; 150
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11-NOV-1999;
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                                                                                                                                                                                                           AAF80150;
284
                                                                                                            RESULT 5
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E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.
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Pred. No. 1.6e-30;
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10.5%; Score 11%; Dest Local Similarity 100.0%; Pred. No. 1.6
Matches 114; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ramirez-Parra E;
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                                                                                                                                                                                                                                                                                                                                     25-SEP-2000; 2000WO-EP009325.
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                                                                                                                                                 Triticum monococcum.
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pharmacogenomic marker; gene;

WO200160860-A2 Homo sapiens.

23-AUG-2001

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

16-MAR-2000; 2000US-0189862P. 25-MAY-2000; 2000US-0207459P. 09-UUN-2000; 2000US-021314P. 18-JUL-2000; 2000US-0219007P.

13-DEC-2000; 2000US-0255281P.

20-FEB-2001; 2001WO-US005171.

17-FEB-2000;

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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they decode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET or by supplementing the patients own production of GENSET or own genes and preventing their expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide con the present sequence is a GENSET nucleic acid of expression and activity. The present sequence is a GENSET nucleic acid of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; gene therapy; vaccine; treatment; diagnosis; GENSET; ss.
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v 100.0%; Pred. No. ...
o; Mismatches
                                                     Human secreted protein cDNA, SEQ ID NO: 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 753; 921pp; English
                                                                                                                                                                                                                                                       07-DEC-2000; 2000WO-IB001938
                                                                                                                                                                                                                                                                                            08-DEC-1999; 99US-0169629P
06-MAR-2000; 2000US-0187470P
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                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                         2001-367870/38
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                                                                                                                                                                                                                                                                                                                                                 (GEST ) GENSET,
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                                                                                                                                             Homo sapiens
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                 11-SEP-2001
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; pituitary; pituitrone; therapy; immune disorder; anaemia; Digeorge syndrome; haematopoietic cell; ataxia telangiectasia; Wiskott-Aldrich disorder; blood coagulation disorder; Addison's disease; autoimmune disorder; multiple selrossis; systemic lupus erythematosus; SLB; hyperproliferative disorder; gene therapy; neoplasm; infectious disease; immunomodulatory; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%; Score 55; DB 5; Length 376;
100.0%; Pred. No. 6.8e-10;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 11212; 11750pp; English.
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Matches
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Gaps

Location/Qualifiers

Key

24-SEP-2001; 2001US-00960352.

99US-0115707P

12-JAN-1999;

11-JAN-2000; 2000US-00480902

(BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.

(MATH/) MATHIALAGAN (TAON/) TAO N. (WARR/) WARREN W C.

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The present sequence is a cDNA encoding rat pituitary hormone, pituitrone. Pituitrone is highly expressed in pituitary gland and is also expressed in brain tissues, spinal cord and kidney. It may be used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate pituitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of haematopoietic cells (e.g., anaemia, blood coagulation disorders, autoimmune disorders (e.g., Addison's disease, multiple sclerosis and systemic lupus erythematosus (SLE)), hyperproliferatiple aclarosis and systemic lupus erythematosus (SLE)), hydiscoliferatiple aclarosis and systemic lupus erythematosus (SLE) (SLE) (SLE) (SLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a novel pituitary hormone (pituitrone), useful for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine EST associated with lactation/muscle/fat deposition #7492.
                              /*tag= a
/product= "Rat pituitary hormone, pituitrone"
/note= "Does not include start codon"
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100.0%; Pred. No. 6.7e-10;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 396 BP; 110 A; 135 C; 91 G; 60 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 269; 277pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-2000; 2000WO-US011211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0131966P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-687547/67.
P-PSDB; AAY71961.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM, Ni J;
                                                                                                                                                                                                                                                   WO200066778-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1999;
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CDS
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The invention relates to a purified nucleic acid molecule associated with

Claim 2; SEQ ID NO 7492; 245pp; English

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

Warren WC;

Tao N,

Byatt JC, Mathialagan N,

WPI; 2003-110599/10.

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The INVENTION Fractives to a purilied nuclear data movestical actation or muscle and fat deposition (designated IMFD), derived from cattle, and the IMFD nucleic acid can specifically hybridise to a second cattle, and the IMFD nucleic acid can specifically hybridise to a second content acid as a ABX34036-ABX49347, or complements of them. Also included are appearing as ABX34036-ABX49347, or complements of them. Also included are included as a promoter and a 3' non- translated sequences that the call to cause termination of transcription and addition of the call to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or the complement of the complementary nucleic acid permits the detection of the molecule. The IMFD nucleic acid, where the detection of the complementary nucleic acid permits the detection of the molecule. The IMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breather in improving cattle. The present sequence is one of the congeneral properation of constructs for use in cattle gene expression, or congenerally improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Scor.
100.0%; Pred. No. o...
0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 10986.
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Best Local Similarity 100.
Matches 55; Conservative
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ID AAI9
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US2002137139-A1.

Bos Taurus

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26-SEP-2002

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polymucleotides obtained from adult testes, foetal brain, adult brain, brain (foetal and adult), foetal kidney, adult spleen, and adult thymus const libraries. The polymucleotides and proteins are predicted to have const libraries. The polymucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haemactopoiesis regulating activity, to activity, haemactopoiesis regulating activity, chemotactic/chemokinetic activity, activin/linhibin activity, chemotactic/chemokinetic activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also grated to be useful for gene therapy. Therapeutic compositions are also presently valuable for veterinary applications. AAZ5281 compositions capted thuman secreted proteins, and AAY73390 to AAX73500 represent human secreted proteins, given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidathmatic; antirknematic; antiarthitic; antivirial; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides and proteins having biological activities which make them suitable for treating, preventing or ameliorating medical conditions in humans or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes human secreted proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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100.0%; Pred. No. 6.4e-10;
htive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              Clark HF, Fechtel K, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 200; Page 702; 730pp; English.
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                   98US-0099950P.
98US-0100424P.
98US-0102329P.
98US-0103615P.
98US-0111799P.
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99US-00248059.
99US-00287150.
  98US-0099843P
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                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
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nes 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-053095/04.
P-PSDB; AAY73485.
                                                                                                                                                                                                                                    13-MAY-1999;
                                                                      29-SEP-1998
                                                                                                               11-DEC-1998
14-DEC-1998
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                          11-SEP-1998
15-SEP-1998
                                                                                                                                                                31-DEC-1998
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                                                                                                                                                                                                            06-APR-1999
                                                                                                                                                                                                                                                                                                                              Wong GG,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to ytyckine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or activin/inhibin activity and may be useful in the diagnosis and/or inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein clone yd261_1 nucleotide sequence SEQ ID NO:191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; immunostimulatory; haemostatic; cytokine;
proliferative; differentiative; chemotactic; chemokinetic; vaccine;
thrombolytic; antiinflammatory; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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100.0%; Pred. No. 6.5e-10;
vative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ52570 standard; cDNA; 491 BP
                                                                                                                                   26-FEB-2001; 2001WO-US004927
                                                                                                                                                                               28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                                                   Tang YT, Liu C, Drmanac RT
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                                                                                                                                                                                                                                                                                                                                               2001-514838/56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAO10995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; ss.
                                      WO200164835-A2.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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17-AUG-1998;
                                                                                       07-SEP-2001
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Query Match

Matches

ઠ 셤 RESULT 12 AAZ52570

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10-JUN-2004

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ARB43398 to ARB44319. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antidathetic; coagulant; nootropic; vasotropic; antipsoriatic and antidanglogenic. Therating or polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAA44420 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC77607 to AAC78448 encode the human cancer associated proteins given in
                                                                                                                                                                                                                                                                                                                                                                         isolated nucleic acids comprising sequences encoding peptides 1 for treating or diagnosing e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 632; 2352pp; English
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                                                                                                                                                       08-MAR-2000; 2000WO-US005882
                                                                                                                                                                                             99US-0124270P
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                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                           Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                WPI; 2000-587533/55
                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB43426.
                                                                           WO200055350-A1
                                                                                                                                                                                           12-MAR-1999;
                                    Homo sapiens
                                                                                                                  21-SEP-2000
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   Gaps
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AAC58600

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soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                      Human soft tissue sarcoma-upregulated DNA - SEQ ID 5349.
                                     (first entry)
                                     26-AUG-2004
                                                                                                       Homo sapiens
                   ADQ22529;
BXSXXXXXXXXXX
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WO2004048938-A2

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                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual
                                                                                                                                                                                                                                                                                                                                                                                                                               which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the
                                                                                                                                                                                                                                                                   Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification per se but was submitted in CD format by the inventor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 5349; 210pp; English.
                                                                                                                                                                                   Zlotnik A;
                                                                                                                                            (PROT-) PROTEIN DESIGN LABS INC.
                                                            26-NOV-2003; 2003WO-US038193.
                                                                                                     2002US-0429739P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 55, Conservative
                                                                                                                                                                                     Ginsburg WM,
                                                                                                                                                                                                                               WPI; 2004-441208/41.
                                                                                                     26-NOV-2002;
                                                                                                                                                                                     Aziz N,
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Human; immune related disease; diagnosis; antiinflammatory; cardiant;

Mermatological; antiarthritic; antirheumatic; immunosuppressive;

Manedostatic; antithyroid; antidabetic; mootropic; neuroprotective;

Mantianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;

Matianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;

Matianaemic; systemic lupus erythematosus; rheumatoid arthritis;

Mateoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;

Matiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;

Matioimmune thromboortyopaenia; immune-mediated renal disease;

Mantioimmune disease; hepatobiliary disease; Mhipple's disease;

Mantioimmune disease; immune-mediated skin disease;

Mattoimmune disease; immune-mediated skin disease;

Mantioimmune disease; irransplantation associated disease;

Mantioimmune mediated skin disease; allergic disease;

Mantioimmune mediated skin disease; allergic disease;

Mart rejection; graft-versus-host-disease; ss. Human PRO1083 protein UNQ540 encoding cDNA SEQ ID NO:116. AAC58600 standard; cDNA; 3759 BP. 29-JAN-2001 (first entry) AAC58600; 

WO200053758-A2 Homo sapiens.

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99US-0123618P.
99US-0123957P.
99US-0125775P.
99US-0128849P.
                                                                  99US-0131445P.
99US-0132371P.
99US-0134287P.
                  02-MAR-2000; 2000WO-US005841
                                                             99WO-US008615
                                                                                            99US-0141037P
                                                                                                 99US-0144758P
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                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                       WPI; 2000-572271/53.
P-PSDB; AAB33435.
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                                    10-MAR-1999;
12-MAR-1999;
23-MAR-1999;
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      14-SEP-2000
                                                       12-APR-1999
                                                                   28-APR-1999
04-MAY-1999
                                                                                                                           08-SEP-1999
                                                                                                                     01-SEP-1
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                                                                                                                                             -SEP-1
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1090.

Gurney AL, Hebert C, Henzel W; D, Shelton DL, Smith V; Wood WI, Yan M; Baker KP, Goddard A, Lu Y, Pan J, Pennica umas D, Watanabe CK, Ashkenazi AJ, Baker KE Kabakoff RC, Lu Y, Pa Stewart TA, Tumas D,

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 23; Fig 43; 309pp; English

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins with PRO anti-PRO ANTI-PRO

ö graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polymucleotide and protein sequences given in the exemplification of the present invention diseases of the lung, and transplantation associated diseases including Gaps ö Sequence 3759 BP; 774 A; 1205 C; 970 G; 810 T; 0 U; 0 Other; Ouery Match 5.1%; Score 55; DB 3; Length 3759; Best Local Similarity 100.0%; Pred. No. 4e-10; Matches 55; Conservative 0; Mismatches 0; Indels 88888888888ద ò

Search completed: February 6, 2005, 17:35:48

Job time : 704 secs

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Sequence 29, Appl Sequence 13, Appl Sequence 13, Appl Sequence 482, App Sequence 482

Title: Perfect score:

Sequence:

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Scoring table:

Word size :

Searched:

Database:

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Sequence 36465, Application US/10425115

Sublication No. US20040214272A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: A Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: OF INVENTION: NUCLEIC Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: NUCLEIC Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: NUCLEIC Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
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                                                         US-09-978-295A-482
US-09-978-192A-482
US-09-998-182A-482
US-09-998-182A-482
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US-09-978-183A-482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), OTHER INFORMATION: Clone ID: MRT4577_133259C.1
US-10-425-115-36465
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TYPE: DNA
ORGANISM: Zea mays
RESULT 2
US-09-731-872-192
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 Query Match
Best Local S:
Matches 59
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Sequence 192, App
Sequence 192, App
Sequence 184240,
Sequence 52629, A
Sequence 7492, Ap
Sequence 7492, Ap
Sequence 122506,
Sequence 123506,
                                                                                                           6, 2005, 17:39:42; Search time 690 Seconds (without alignments) 9084.062 Million cell updates/sec
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                                                                                                                                                                                                                Description
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Compugen Ltd.
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US-09-876-997-192

US-09-876-997-192

US-10-425-115-184240

US-10-425-115-150417

US-10-425-115-52629

US-10-950-352-7492

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               version :
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Gapop 60.0 , Gapext 60.0
             GenCore
Copyright (c) 1993
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Maximum DB seq length: 200000000
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Match
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Sequence Sequence

Sequence Sequence

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Gaps

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Result 8 8 9 11

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Sequence 150417, Application US/10425115
Sequence 150417, Application US/10425115
Fublication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Las Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Yongui
APPLICANT: Shou, Yihua
APPLICANT: Con, Yongui
APPLICANT: Con, Yongui
APPLICANT: Shou, Shou
                                                                                                                                                        APPLICANT: La Rovalitus:
APPLICANT: La Rovalit, David K.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yinua
APPLICANT: Shou, Yongwei
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SUMBER OF SEQ ID NOS: 369326
SEQ ID NO 184340
LENGTH: 2121
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18-10-425-115-52629, Application US/10425115

18-10-425-115-52629, Application WS/10425115

18-10-425-115-52629, Application No. US20040214272A1

18-10-425-115-52629, Application No. US20040214272A1

18-10-425-115-52629, Application No. US20040214272A1

18-10-425-115-52629, Application No. US200402142A1

18-10-425-115-52629, Application US/10425115

18-10-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425-115-425
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100.0%; Pred. No. 1.6e-17;
ive 0; Mismatches 0;
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) OTHER INFORMATION: Clone ID: MRT4577_68706C.1
US-10-425-115-150417
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; OTHER INFORMATION: Clone ID: MRT4577_99614C.1
US-10-425-115-184240
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                                          Sequence 184240, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.1%
Best Local Similarity 100.0°
Matches 56; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-425-115-150417/c
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                                                                                                                       APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: JOBERT, Severin
TITLE OF INVERTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR PILING DATE: 2000-12-08
PRIOR PILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 192
LENGTH: 668
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APPLICANT: Dungs Milne Edwards, Jean Baptiste
APPLICANT: Dobert, Lydie
APPLICANT: Dobert, Severin
TITLE ON TOBERT, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US4.CIP
CURRENT APPLICATION NUMBER: US/09/876,997
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/131,872
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.1%; Score 56; DB 9; Length 668; 100.0%; Pred. No. 1.6e-17;
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Sequence 192, Application US/09731872
Patent No. US20020102604A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US.09-876-997-192
; Sequence 192, Application US/09876997
; Publication No. US20030152921A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 56; Conservat
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; LOCATION: 57..203
US-09-731-872-192
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; LOCATION: 57..203
US-09-876-997-192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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RESULT 4

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Length 538
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                                                                                                                                                                                                                                                          TYPE: DNA COTHER INFORMATION: Clone ID: 32-LIB34-017-Q1-E1-H7
                                                                                                                                                                                                                                                                                                                                                                               5.1%; Score 55; DB 9; Lilarity 100.0%; Pred. No. 5.1e-17; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 5.1e-17;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_183771C.1
US-10-425-115-91860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 91860, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 55; Conserv
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Best Local Similarity
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-425-115-91860/c
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                                                                                                                                                                                                                                                                                                          DB 18; Length 369; 5.1e-17;
                                                                                                                                                                                                                                    ) OTHER INFORMATION: Clone ID: MRT4577_147996C.1
US-10-425-115-52629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: IDENTIFICATION, ASSESSMEN
TITLE OF INVENTION: IDENTIFICATION, ASSESSMEN
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-55
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/215,281
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                          5.1%; Score 55; DB 100.0%; Pred. No. 5.1. ive 0; Mismatches
                   FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 52629
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 58429, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
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Patent No. US20020137139A1
GRNEAL INFORMATION:
APPLICANT: Warren, Weeley C.
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.C
Matches 55; Conservative
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                               TYPE: DNA ORGANISM: Zea mays
TITLE OF INVENTION:
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US-09-960-352-7492/c
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US-10-357-930-58429
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APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERBNCE: 16511.006/37-21 (10298) C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 7492
LENGTH: 410
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Sy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION: DAG VONGREI: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 122506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa, Thomas J.
APPLICANT: Cavalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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NAME/KEY: CDS
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APPLICANT: Rovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Youngei
TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
SEQ ID NO 163680
LENGTH: 838
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Patent No. US2002052308A1

GENERAL INFORMATION:

APPLICANT: ROBER and Antibodies

FILE REFERENCE: PA106

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PatentIN Ver. 2.0

LENGTH: 917
                                                                                                                                       Query Match 5.1%; Score 55; DB 17; Length 787; Best Local Similarity 100.0%; Pred. No. 5.2e-17; Matches 55; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.1%; Score 55; DB 18; Length 838; Best Local Similarity 100.0%; Pred. No. 5.2e-17; Matches 55; Conservative 0; Mismatches 0; Indels
                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_81629C.1
US-10-424-599-122506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_80852C.1
US-10-425-115-163680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(838)
OTHER INFORMATION: unsure at all n locations
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Publication No. US20040214272A1
GENERAL INFORMATION:
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                    TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
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US-09-925-301-29
LENGTH: 787
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US-VB-BUB-3-89-13

Sequence 13, Application US/09803589

Patent No. US2002012251A1

GRENERAL INFORMATION:

APPLICANT: MCCARTHY, Sean A.

APPLICANT: HOLTZMAN, DOUGlas A.

APPLICANT: GROGGARI, Andrew D.A.

TITLE OF INVENTION: PROGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: NOVER: USES

FILE REFERENCE: 07334-32501

CURRENT APPLICATION NUMBER: US 09/120,99

PRIOR APPLICATION NUMBER: US 09/130,491

PRIOR APPLICATION NUMBER: US 06/054,665

PRIOR APPLICATION NUMBER: US 06/054,966

PRIOR FILING DATE: 1998-08-06

PRIOR FILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 13

LENGTH: DATE: 1027
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Publication No. US2004025365A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
APPLICANT: Holtman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
ITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER TITLE OF INVENTION: USES
FILE REPERENCE: 07334-325601
CURRENT PELLING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: US/10/718,332
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: US/09/803,589
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  Length 917;
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                                                        Indels
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Best Local Similarity 100.0%; Pred. No. 5.2e-17;
Matches 55; Conservative 0; Mismatches 0;
Query Match 5.1%; Score 55; DB Best Local Similarity 100.0%; Pred. No. 5.2 Matches 55; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (106)...(630)
US-09-803-589-13
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us-10-088-830-1.oli.rnpb

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Sequence 5349, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INPORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Glabburg, Wendy M.
; APPLICANT: Clotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TILLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: 108/10/723,860
; CURRENT APPLICATION NUMBER: 60/429,739 ·
PRIOR APPLICATION NUMBER: 60/429,739 ·
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5349
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PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/128,709
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 60/054,645
PRIOR PILING DATE: 1999-0-04
PRIOR PILING DATE: 1998-08-06
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-01
PRIOR FILING DATE: 1999-09-01
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PRIOR FILING DATE: 1999-09-01
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: DCATION: (2063) ..(2063)

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US-10-723-860-5349
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; LOCATION: (106)...(630)
US-10-718-332-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Mus musculus
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ORGANISM: Homo sapiens
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Search completed: February 6, 2005, 21:54:29 Job time : 692 secs

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Sequence Populus

Perfect score:

Sequence:

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Scoring table:

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AX449314 Sequence
BC013193 Homo sapi
BC013993 Homo sapi
CQ717592 Sequence
AR380911 Sequence
U18422 Homo sapien
BC082841 Xenopus 1
AX333694 Sequence
CQ48916 Sequence
CQ48916 Sequence
BC080383 Xenopus 1
AX449515 Sequence
AX008165 Caenorhab
CQ581589 Sequence
AY008165 Caenorhab
CQ581589 Sequence
AY003183 Drosophila
AY065526 Drosophil
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Pooideae, Triticeae, Triticum.
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/note="unnamed protein product"

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AX2111611 C

AX100712 S

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AX100714 S

BT005286 A

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AX117135 A

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AX120207 S

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Compugen Ltd.
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                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                          Ramirez-Parra, E. and Gutierrez, C. Characterization partner of the Characterization of wheat DP, a heterodimerization partner of the plant E2F transcription factor which stimulates E2F-DNA binding FEBS Lett. 486 (1), 73-78 (2000)
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/db xref="taxon:4569"

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/en. .13

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/function="cell cycle E2F dimerization partner"

/function="cell cycle E2F dimerization partner"
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Submitted (03-FEB-2000) Gutierrez C., C.S.I.C.-U.A.M.,
Biologia Molecular, Cantoblanco, Madrid 28049, SPAIN
Location/Qualifiers
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sp. mRNA for DP protein (dp gene).
                                                          Triticum sp. mRNA for DP protein 4M271917
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Pgene, E2F dimerization partner. Triticum sp.
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Gutierrez, C.
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Oryza sativa (japonica cultivar-group) cDNA clone:J013105118, full insert sequence.

DEFINITION

AK111611.1 GI:37988274

ORGANISM VERSION KEYWORDS SOURCE ACCESSION

REFERENCE

FLI\_CDNA; CAP trapper.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

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Volin, M., Mayazaki, S., Shiraki, T.,
Volin, M., Shiraki, T.,
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Nadada,T., Kawagashira,N., Doi,K., Kibhimoto,N., Yazaki,J.,
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Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
Masuda,H., Mutra,J., Mizuno,K., Narikawa,R., Nikhura,J., Oka,M.,
Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,R. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Alzawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Harao,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice Science 301 (5631), 376-379 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (12-58P-2002) Shoshi Kikuchi, National Institute of Submitted (12-58P-2002) Shoshi Kikuchi, Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 205-802. Japan (E-mail:8Kluchi@mias.affrc.go.jp, 7007, Fas.81-29-838-7007, This clone is one of the 32K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshino, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 1174)
Kikuchi, S.
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LRNQAGORPAESVYDILLPFLLIKTSRKARVEIEISESBKFARFDFNGAPFTWHDDVS
ILEAIRRNKGRAGLSIHP"
                                                                           05-FEB-2004
protein
                                                                                                                                       942 TITIAACCIGCAAAITITIGICICCTITITIGIGCCIAGCAGGITATIAGGICICAGAIAGA 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
        931 TGTCAAAACTCAAAACTGGCACCACCAGTTTCTTTGCACAGTTATGTATAGCTATAGCG 990
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CA 92121,
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                                                       ----TATCCTCATGAAAACTTGACCTAGTTTATAGGACAGTCTCTCAGGCTTGAGAAGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:39947"
/note="derived from yeast two-hybrid experiments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coper, B., Hutchison, D., Park, S., Guimil, S., Luginbuhl, P., Ellero, C., Goff, S. and Glazebrook, J. Direct Submission
Submitted (23N-22003) Torrey Mesa Research Institute, Sy Research and Technology, 3115 Merryfield Row, San Diego, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (japonica cultivar-group)
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Pred. No. 4.6e-87;
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/product="DP protein"
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/db_xref="GI:29367575"
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/organism="Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="Nipponbare"
/isolate="21044"
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larity 79.8%;
Conservative 0
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Best Local Similarity
Matches 548; Conserv
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JOURNAL
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KEYWORDS
SOURCE
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AY224529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAAGCGGGCGGTAATGCGGTCCAAAGGAAGGGGCTGTTGACCCGGATAAAGATAGGAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAAGTTCACAAAGAACTCATCACCAGGATCAAGAATAAGAAGAAGCTTCTCCAGGAAAT 633
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Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakkamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M.,
Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Shibata, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M.,
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Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Yasunishi, A. and Hayashizaki, Y.
Yasunishi, A. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 515; DB 8; Length 117
Pred. No. 4.1e-103;
0; Mismatches 185; Indels
                                                                                                                                                                                                                                                                        /organism="Oryza sativa
                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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ilarity 77.4%;
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/proteIn_id="CAC36471.1"
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IRLPFVLVKTSR"
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Triticum monococccum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 CGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA
                                                                                                             317 ATGGCACATATTGGTCAAGGGTTTGATGAGAATATTAGGCGGAGAGTGTATGATGCT
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                                                                                                                                                                                                                                                       437 GGCCTTTCAAATTACAGATATGAAAAATAAAGAAGCTTGAGGAAGTT 484
                                     Length 168;
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BT005286
BT005286.1 GI:28950852
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Gutierrez-Armenta, C.C. and Ramirez-Parra, B.C.
Wheat dp proteins and uses thereof
Patent: WO 0121644-A 11 29-MAR-2001,
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS
Location/Qualifiers
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                                     15.4%; Score 168; DB 6; I
100.0%; Pred. No. 1.3e-26;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.3e-26;
iive 0; Mismatches 0;
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/note="unnamed protein product"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Triticum monococcum"
/mol_type="unassigned DNA"
/db_xref="taxon:4568"
                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                          Sequence 11 from Patent WO0121644.
AX100714
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Best Local Similarity 100.
Matches 168; Conservative
                                                                          Conservative
                                   Query Match
Best Local Similarity
Matches 168; Conserv
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YRYEKIKKLEEV"
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Triticum monococcum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
TITICGGAGCTGAAGTCCATTACGCAGAACGGTCTGGAGTTTGATGAGAAGAATATTAG 440
                                                                                                                                                                                                                         GCGGAGGGTATATGATGCTTTCAATGTGCTCATTGCAATTCGTGTTATTGCAAAAGATAA 500
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                                                                                                                            TTATTCAGAGCTGAAGTCCATGGCACATATTGGTCAAGGGTTTGATGAGAAATATTAG 357
                                                                                                                                                                                                 GCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAAGAAAA 417
                                                                                                                                                                                                                                                                        CGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTC 597
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                                                       AGTITGTGAGAAAGTIGAAGCCAAAGGAAGAACAACAIACAAIGAGGIIGCAGACGAAAI
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Patent: WO 0121644-A 9 29-MAR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS
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/mol_type="unassigned DNA"
/db_xref="taxon:4568"
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/protein_id="CAC36470.1"
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AX100712.1 GI:13619660
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ATH319027 960 bp mRNA linear PLN 29-JAN-2002 Arabidopsis thaliana partial mRNA for E2F dimerisation partner protein (dp2a gene).
                                                                                                                                                                                                                                                                                                  251 GTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 GCCACAATTAAGCAAAACGCAGAGAAGCCTTTGAATGAAATGAGTACAATGAGAAGAAC 312
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Submitted (29-AUG-2001) Bergounioux C., UMR 8618, Cnrs, IBP bat
Universite Paris-Sud, 91405 Orsay, FRANCE
Location/Qualifiers
1..960
                                                                                                                                73 ACTCCAGTGAGAAGGAAATTGATTGTTGATGATGATTCTGAAATTGGATCAGAGAAA
                                                                            131 AATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGAAGGCT
                                                                                                                                                                                                                                                                                                                                  193 TTGGAAGCCAAGAAGAAAACTACTACAAGGAGGTTGCAGACGAAATTATTCAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                            311 AAGTCCAT-------GGCACATATTGGTCAAGGTTTGATGAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA
                                                                                                                                                                                         191 GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGAAAAATAGTTTGTGAGAAA
                                                                                                                                                                                                                                         GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG
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dp2a gene; E2F dimerisation partner protein.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embr
Pred. No. 2.3e-23;
0; Mismatches 259;
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Best Local Similarity
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/brotein id="AA063350.1"
/bratein id="AA063350.1"
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GQSRTSGGGLRQFSVMVCQKLEAKKITTYKEVADEIISDFATIKQNAEKPLNENEYNE
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AFLKELREKYGSLESIMSRNORMVVKTQGPAGGFTLPFILLETNPHAVEIESBOWG
LVHLDFNSTPFSVHDDAYILKLMQEQKQEQNRVSSSSSTHHQSQHSSAHSSSSSCIAS
GTSGPVCWNSGSIDTR"
                                                                                                   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 879)
Chan, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wau, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 879)

(Chan, M.W., Chenk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M.W., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kanaya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Ondera, C.S., Pallm, C.J., Quach, H.L., Sakurani, T., Sakurani, R., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-MAR-2003) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collection and clustering of RAFL cDNAS (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members constructed and agequenced the pUNI (ORF) clones using the RAFL CDNAB: Kin, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M., Dale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B., Chee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and
                                                                               Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally
this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
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'note="putative DP-2 transcription factor"
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/note="This clone is in pUNI 51"
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                         Arabidopsis thaliana (thale cress)
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source

Length 879;

8

B

Score 153.6;

14.18;

Match

Query

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PAT 03-JUL-2002
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                                                                                                                                                                                                Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                       , Boudolf, V., de Veylder, L., Acosta, J.A. and Magyar, Z. acid molecules encoding plant cell cycle proteins and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thaliana"
                                                                                                       DNA
      751 AATAGCACACCTTTCTCGGTCCATGATGAT 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis tha
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
                                                                                                     1114 bp
from Patent W00185946.
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Location/Qualifiers
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GQSRTSGGGLRQFSVWCQKLEAFKTTTYREWADEI1SDFATTKQNARFPLRENEYNE
KNIFRRYYDALNVFWALDIIARDKEIRWKGLPITCKCDVEEVKMDRNKVMSSVQKKA
AFLKELRERVSSLESLMSRNQEMVVKTQGPARGFTLPFILLFTNPHAVVEISSBDMQ
LVHLDFNSTVPFSVHDDAYILKLMQEQKQEQNRVSSSSSTHHQSQHSSAHSSSSSCIAS
GTSGPVCWNSGSIDTR"
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                                                                                                                                                                                                                                                                                                                                      /db_xref="GOA:Q9FNY3"
/db_xref="UniProt/TrEMBL:Q9FNY3"
organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                            /codon_start=1
/product="E2F dimerisation
                                                                                                                                                                                                                                       /function="transcription"
                                                                                                                                                                                                                                                                                               /protein_id="CAC87459.1"
/db_xref="GI:18447786"
            /mol type="mRNA"
/cultivar="Colombia"
/db xref="taxon:3702"
/tissue_type="buds"
/dev stage="flowering"
                                                                                                                                                                       /gene="dp2a"
79 oc7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.1%;
55.6%;
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131 AATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGGAGAAGGCT 190
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                      256 TTGGAAGCCAAGAAAAATAACTACTTACAAGGAGGTTGCAGACGAAATTATTTCAGATTTT 315
                                                                                                                                                                                                                                                                           316 GCCACAATTAAGCAAAACGCAGAGAGCCTTTGAATGAAATGAGTACAATGAGAAGAAC 375
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                          GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA
                                                                                                                           GITGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG
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Nucleic acid molecules encoding plant cell cycle proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1189;
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/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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AX449329
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KNIRRRVYDEJANVYPMALDIIABDKEERWGGLPTICKKOVEBYGDRDKVMSSVQKKA
AFLKELREKVSLESLARNOEMVXTQGPREGFTLPFILLETNPHAVVEIELSEDMO
LVHLDFNSTPFSVHDDAYILKLMQEQKQBQNRVSSSSSTHQSQGSSASSSSCIAS
                                                                                                                                                                       Arabidopsis thaliana At5902470 mRNA for putative DP-2 transcription factor, complete cds, clone: RAFL16-67-D16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     et
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                                                                                                                                                                                                                                                                                                                                                       Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An Arabidopsis full-length cDNA library was constructed essential as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1-B vector (Carninci al. (2001) Genomics 77:79-90) digested with BamHI and SalI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is in a modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seki,M., Iida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
Arabidopsis thaliana full-length CDNA
Published Only in Database (2002)
2 (bases 1 to 112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishida,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:meski@gsc.riken.go.jp, Tel:81-45-503-9625, Fax:81-45-503-9586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida
Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P.,
Kawai, J., Hayashizaki, Y. and Shinozaki, K.
Direct Submission
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protein_id="BAC41813.1"
db_xref="GI:26449372"
                                                                                                                                                     linear
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55.6%; Pred. No. 2.4e-23;
ive 0; Mismatches 259;
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AATAGCACACCTTTCTCGGTCCATGATGAT 715
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/gene="At5g02470/T22P11_60"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/db_xref="taxon:3702"
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Arabidopsis thaliana
Mkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 GCCACAATTAAGCAAAACGCAGAGAAGCCTTTGAATGAAAATGAGTACAATGAGAAGAAC 485
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A method to modify cell number, architecture and yield of plants loverexpressing the e2f transcription factor
Patent: WO 03025185-A 3 27-MAR-2003;
CropDesign N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTTATGTTTTGTCAGAAG
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                                                                 GCGCCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA
                                                                                                                                                      251 GTTGAAGCCAAAGGAAGAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAAAAGGGGGTGGATGGGCCTTTCAAATTACAGATATGAAAAATTAAAGAAG
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Pred. No. 2.4e-23;
0; Mismatches 259;
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/mol_type="unassigned DNA"
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                        GCGCCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACTAGGTTTGTGAGAAA
                                                                                 GGCCAATCAAGAACTTCTGGAGGCGGGCTTTCGTCAATTCAGTGTTATGGTTTTGTCAGAAG
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                                                                                                                          GTTGAAGCCAAAGGAAGAACAACATACAATGAGCTTGCAGACGAAATTTATTCAGAGCTG
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Pred. No. 2.4e-23;
0; Mismatches 259; Indels
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cell cycle

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        ^corganise="Arabidopsis thaliana"
        /mol_type="unassigned DNA"
        /db_xref="taxon:3702"

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Method and means for modulating plant
use in plant cell growth control
Patent: WO 03018818-A 3 06-MAR-2003;
Cropbesign N.V. (BE)
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Sequence 3 from Patent W003018818.
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Direct Submission
Submitted (06-SEP-2000) Magyar Z., Department Plantgenetica,
Submitted (06-SEP-2000) Magyar Z., Department Plantgenetica,
Laboratorium voor Genetica, Universiteit Gent, K.L. Ledeganckstraat
35., B-9000, Gent, BELGIUM
Location/Qualifiers
1. 1274
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                                                                                                                                                                                                                                                              Magyar, Z., Atanassova, A., De Veylder, L., Rombauts, S. and Inze, D. Characterization of two distinct DP-related genes from Arabidopsis
                                                                                               GGGCAATCAAGAACTICTGGAGGCGGGCTICGTCAATTCAGTGTTATGGTTTGTCAGAAG 365
                                                                                                                           GTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG 310
                                                                                                                                                                                                                                                                                                                    GAAATCGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAA---ACACTG 589
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              AATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGAAGGCT 190
                                        ACTCCAGTGAGAAGGAAATTGATTGTTGATGATTCTGAAATTGGATCAGAGAAA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="dpa"
/Ec_number="6.3.2.19"
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                                                                                                                                                                                                                                                                1. - 1274
/gene="dpa"
174. .1052
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Matches 350; Conservative
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PAT 10-APR-2001
                                                                                                     Triticum monococcum
Triticum monococcum
Edwaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
                                                                                                                                                                                           Gutierrez-Armenta, C.C. and Ramirez-Parra, B.C. Wheat dp proteins and uses thereof Patent: WO 0121644-A 7 29-MAR-2001; CONSEJO OUDERLOR BINVESTIGACIONES CIENTIFICAS (ES) Location/Qualifiers
                                linear
                                                                                                                                                                                                                                                                       1. .153
/organism="Triticum monococcum"
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                               AX100710 153 bp
Sequence 7 from Patent W00121644.
AX100710 GI:13619658
RESULT 15
AX100710
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                            source
                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                           FEATURES
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Search completed: February 6, 2005, 14:35:10 Job time : 5151 secs

14.0%; Score 153; DB 6; Length 153; 100.0%; Pred. No. 2.6e-23; tive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.0
Matches 153; Conservative

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0; Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

February 6, 2005, 12:23:21 ; Search time 697 Seconds (without alignments) 9249.065 Million cell updates/sec Run on:

Title: Perfect score:

Sequence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ1980s:\* genesequ1980s:\* genesequ2001as:\* genesequ2001as:\* genesequ2001as:\* genesequ2001as:\* genesequ2003as:\* genesequ2003as:\* genesequ2003as:\* geneseqn2003ds:\* geneseqn2004as:\* geneseqn2004bs:\* geneseqn2003cs: N\_Geneseq\_16Dec04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES æ

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Description	Aaf80144 Nucleotid	Adg36842 Cell prol	Adk71795 Rice endo	Ado63159 Transcrip	Aaf80149 DNA fragm	Aaf80148 DNA fragm	Ado62852 Transcrip	Ado63084 Transcrip	Ado62144 Transcrip	Aas96287 Arabidops	Aas96319 Arabidops	Adh59559 Dimerisat	Acc45100 Arabidops	Ado63626 Transcrip	Aaf80147 DNA fragm	Aaf80146 DNA fragm	Ado63082 Transcrip	Ado62142 Transcrip	Aac39795 Arabidops	Aaf80150 DNA fragm
ID	AAF80144	AD036842	ADK71795	AD063159	AAF80149	AAF80148	AD062852	AD063084	AD062144	AAS96287	AAS96319	ADH59559	ACC45100	AD063626	AAF80147	AAF80146	AD063082	AD062142	AAC39795	AAF80150
DB	4	12	10	12	4	4	12	12	12	9	9	10	10	12	4	4	13	12	m	4
* Query Match Length DB	1089	885	548	548	168	168	1443	1267	1267	1114	1189	1274	1274	1153	153	156	1158	1158	1618	150
% Query Match	9.66	40.6	20.0	20.0	15.4	15.4	14.5	14.3	14.3	14.1	14.1	14.1	14.1	14.1	14.0	13.9	13.8	13.8	13.8	13.8
Score	1084.2	442.2	218	218	168	168	157.6	155.2	155.2	153.6	153.6	153.6	153.6	153.4	153	151.2	150.8	150.8	150.8	150
esult No.	-	7	m	4	ß	9	7	80	σ	10	11	12	13	14	12	16	11	18	13	20

Aaa59702 DNA encod	Ado63363 Transcrip	Aaz34580 Corn DP-2	Add36854 Cell prol	Add36844 Cell prol	Ado63216 Transcrip	Ado62851 Transcrip	Aas96304 Arabidops	Ado63362 Transcrip	Aas96415 Arabidops	Adr65325 Cotton cD	Acn88986 Breast ca	Adi32130 Human cDN	Adn05729 Antipsori	Abl65866 Lung canc	Aas92244 DNA encod	Acn38014 Tumour-as	Abv26838 Human pro	Abv20992 Human pro	Aaz34577 Impatiens	Aas96410 Arabidops	Aas96332 Arabidops	Aav72862 Caenorhab	Abl08071 Drosophil	Aac56435 Pinus rad
AAA59702	AD063363	AAZ34580	ADQ36854	ADQ36844	AD063216	AD062851	AAS96304	AD063362	AAS96415	ADR65325	ACN88986	ADI32130	ADN05729	ABL65866	AAS92244	ACN38014	ABV26838	ABV20992	AAZ34577	AAS96410	AAS96332	AAV72862	ABL08071	AAC56435
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12.7	12.7	12.5	12.5	12.1	11.7	11.3	10.9	10.6	9.6	9.4	9.1	9.1	9.1	8.9	8.9	8.9	8.9	8.9	8.7	9.8	9.8	8.1	8.1	7.8
138.2	138.2	136.6	136.2	132.2	127.8	123	118.6	115	104.6	102.8	99.2	98.8	98.8	97	97	97	97	97	95.2	93.6	93.6	88	88	85
21	22	23	24	25	36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 AAF80144

BP. AAF80144 standard; DNA; 1089

AAF80144;

11-JUN-2001 (first entry)

Nucleotide sequence of a wheat E2F-dimerisation partner (DP) protein.

E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation; 

Triticum monococcum.

Key

Location/Qualifiers
20. 805
A'tags / A
/product= "E2F-dimerisation partner (DP) protein"

WO200121644-A2

29-MAR-2001.

25-SEP-2000; 2000WO-EP009325

99ES-00002127. 99ES-00002474. 24-SEP-1999; 11-NOV-1999; (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.

Gutierrez-Armenta C, Ramirez-Parra E;

WPI; 2001-257972/26. P-PSDB; AAB67762.

New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.

Claim 13; Fig 1; 77pp; English.

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protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be medulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue size
encodes a E2F-dimerisation partner (DP) protein. The
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Sequence 1089 BP; 367 A; 215 C; 261 G; 246 T; 0 U; 0 Other;

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                                                                                                                                   AGCGGGCGGTAATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAGGAAGAA 180
                                                                                                                                                                                                                                                                                                   GCACAAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACACAAATAGT 240
                                                                                                                                                                                                                                                                                                                                                                                                      TTCAGAGCTGAAGTCCATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u> aaaacagiriigaigaiciccaaaacaicaagiracgiaaccaaacaciggaaagcicagc</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGAATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTGGCCGCCCCCCTTCACTAGAGACTCAAGAATATTACAAATGAATTAAAAAGGTTT
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                                                                                                                                                                                                                                                                    GGAGAAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGT
                                                                                                                                                                                                                                                                                                                                    TTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTA
                                    Gaps
 Length 1089;
                                  ö
                                  3; Indels
 DB 4;
 Score 1084.2; DB 4
Pred. No. 5.2e-207;
                                  0; Mismatches
99.68;
                   Best Local Similarity 99.7
Matches 1086; Conservative
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   Query Match
Best Local
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1020
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                                                                                                                   1020
                                                                                                                                         960
                      900
                                                                                                                                                                                                                                                                                                                                                                 cell proliferation; senescence;
              CTTGACCTAGTTTATAGGACAGTCTCTCAGGCTTGAGAAGATTTTAACCTGCAAATTTTG
                                                                                            AGAACTGGCACAGCCGGATTCTTTTGCACAGCTATGTATAGCTATATATCCTCATGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to an isolated nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and f producing enhanced food crops.
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                                                                                                                                                                                                                                                                                                                                           Cell proliferation-related nucleic acid sequence #1.
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                                                                                                                                                                                                                                                                                                                                                                  related polypeptide;
ress response; ds.
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                                                                                                                                                                                                                                                                                                                                                                     cell proliferation related polypep
differentiation; stress response;
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                                                                                                                                                                                                                                                                         ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-2003; 2003WO-US041200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2002; 2002US-0436565P
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                                                                                                                                                                                                                                                                          882
                                                                                                                                                                                                                                                                          ADQ36842 standard; DNA;
                                                                                                                                                                                                               AAAAAAAA 1089
                                                                                                                                                                                         AAAAAAAA 1089
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Query Match
40.6%; Score 442.2; DB 12; Length 885;
Best Local Similarity 79.8%; Pred. No. 8.7e-79;
Matches 548; Conservative 0; Mismatches 133; Indels 6;

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The present invention describes rice endosperm specific expression sequence labels (expressed sequence tag (BST)) comprising the 48 CDNA sequence, given in SEQ ID NO:1 to 48. The expression sequence labels can be combined in a gene chip using the microarray technique. The expression sequence labels are useful for DNA sequence determination of constitutive rice endosperm CDNA library, removing redundant sequences, and searching interconnection network data bases. The chip can be used for gene cloning, early prediction of hybrid vigour, safety detection of transgenic agricultural product, screening new-type herbicides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATITICGGAAGATICAAAGITITGCACGCTICGACTICAACGGIGCACCATICACCATGCA 179
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                                                                                                        expression sequence labels useful for
                                                                                                                                                                                                                                                                                                                                                                               Sequence 548 BP; 164 A; 118 C; 112 G; 154 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 218; DB 10;
Pred. No. 4.8e-34;
0; Mismatches 140;
                                                                                                                                                      Claim 1; SEQ ID NO 31; 28pp; Chinese.
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nilarity 71.1%;
Conservative 0
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                                                                     WPI; 2003-301573/30
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Best Local Similarity
Matches 391; Conserv
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                                                                                                                                   AGTTTGTGAAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAAT
                                                                                                                                                                                                                                      TTTTGCGGAGCTGAAGTCCATTACGCAGAACGCTCTGGAGTTTGATGAGAAGAATATTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice endosperm expressed sequence tag (EST) SEQ ID NO:31
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Claim 1; SEQ ID NO 1626; 510pp; English.
                                                                                                    Heard JE, Ratcliffe O, C
JL, Haake V, Dubell AN,
                                                                                            (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                            18-SEP-2002; 2002US-0411837P.
17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                    18-SEP-2003; 2003WO-US030292.
       (first entry)
                                                                                                                WPI; 2004-330163/30.
                                                    WO2004031349-A2.
                                                                                                    Jiang C, Heard
Riechmann JL,
       15-JUL-2004
                                                            15-APR-2004
ADO63159
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E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                    60 GGCATCCTCCTTCCGGTTCTTATTGATCAAGACATCCCGAAAAGCAAGGCTGGAAATTGA 119
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                                                                                                                                                                                                 554 GATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAGAATGTTAAT
                                                                                                                                                                                                                                                      1 GACCTTCCAGAATATACATTACGCAACCAGGCTAGTCAGAGGCCCA-CAGAAAGTGTTAAT
                                                                                                                                                                                                                                                                                                              614 GGCATCCGCCTTCC-ATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTGGAAATTGA
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                                                                                Length 548;
                       C; 112 G; 154 T; 0 U; 0 Other;
                                                                                                                                        Indels
                                                                                DB 12;
                                                                             20.0%; Score 218; DB 12; ilarity 71.1%; Pred. No. 4.8e-34; Conservative 0; Mismatches 140
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                       Sequence 548 BP; 164 A; 118
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11-NOV-1999;
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                                                                                                                                                                   Plant; transcription factor; transgenic plant; abiotic stress tolerance; semblic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low hosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides, useful for producing transgenic plants with advantageous
properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reuber TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention relates to novel plant transcription factor
                                                                                                             Transcription factor G2981 orthologous sequence, SEQ ID 1626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adam LJ, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant polynucleotide encoding transcription factor
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Keddie JS,
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AAF80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell progression. E2F and retinoblastom of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a heterobinder in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be medulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant; transcription factor; transgenic plant; abiotic stress tolerance; somedic stress tolerance; old tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 ATGGCACATATTGGTCAAGGGTTTGATGAGAATATTAGGCGGAGAGTGTATGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Argecacararregreaaggerrrgargaagaararraggegagagagrerrgarger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.4%; Score 168; DB 4; Length 168; 100.0%; Pred. No. 3.7e-24; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTTTCAAATTACAGATATGAAAAAATAAAGAAGCTTGAGGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437 GGCCTTTCAAATTACAGATATGAAAAAAAAAAAAGAAGCTTGAGGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 168 BP; 59 A; 19 C; 44 G; 46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang C, Heard JE, Ratcliffe O, Creelman RA, Riechmann JL, Haake V, Dubell AN, Keddie JS,
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 73-74; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEND-) MENDEL BIOTECHNOLOGY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-2002; 2002US-0411837P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2003; 2003US-0465809P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 168; Conservative
                                                           WPI; 2001-257972/26.
P-PSDB; AAB67766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004031349-A2.
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                  THE CANAGE OF THE PROPERTY OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblactoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblactoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly organ or tissue size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGTITGAIGAICICCAAAACAICAAGTIACGIAACCAAACACTGGAAAGCTCAGCAGAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E2F-dimerisation partner, DP protein, E2F transcription factor, G1 phase, S phase, cell cycle, retinoblastoma protein, alter cell proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGITIGALGATCTCCCAAACAICAGITACGIAACCAAACACGGAAAGCICCAGCAGAG 604
                                                                                                                                                                                                                                                                                                           New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.4%; Score 168; DB 4; Length 168; 100.0%; Pred. No. 3.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATGITAAIGGCAICCGCCTTCCATTCGTATTGGTCAAGACAICTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 168 BP; 62 A; 38 C; 33 G; 35 T; 0 U; 0 Other;
(CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
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                                                                                            Ramirez-Parra E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 74-75; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gutierrez-Armenta C, Ramirez-Parra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF80148 standard; DNA; 168 BP.
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99ES-00002474
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Matches 168; Conservative
                                                                                            Gutierrez-Armenta C,
                                                                                                                                                                               WPI; 2001-257972/26.
P-PSDB; AAB67767.
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11-NOV-1999;
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Reuber TL;

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CATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTGGAAATTGAGAT

CCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAGAATGTTAAT---GG

559

919

737 TGTATCTTTACCCTTTATTTTGGTACAGACGTCCTCATGCAACTGTGGAAGTGGAAAT 796

797 Arcadaadarardcadcrigricarrirdarrirdaaradcacrecrirraagcrigcarda 856

736 TGATCTCTCAATCCTTGAGG 755 ccacaarrarcricrcaacc 876

857

TTCAGATGACTCGAAGTTTGCCCCATTTCGAGTTCAATGGTGCACCATTCACATTGCATGA

919

Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.

Arabidopsis thaliana.

WO2004031349-A2.

15-APR-2004

Transcription factor G2982 coding sequence, SEQ ID 1551.

(first entry)

15-JUL-2004

ADO63084;

BP.

ADO63084 standard; DNA; 1267

919

617 GAATAGAATTGAAAAGAAAACAGCCTATCTGCAGGAGCTTGAGGAGCAATTCGTAGGTCT

CAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAACAGTTTGATGATCT

557 499

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us-10-088-830-1.rng

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The present invention relates to nove! plant transcription factor proteins (I) and nucleotide sequences (II) (Abo61574-Abo63778). The present invention relates to nove! plant transgenic plant be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a altered trait selected from increased tolerance to abicits stress, increased tolerance to conditions, increased tolerance to conditions, increased tolerance to conditions, increased tolerance to classes, increased tolerance to conditions, increased tolerance to disease, including clusphate conditions, increased tolerance to disease, including clusphate conditions, increased tolerance to disease, including clusphate conditions, increased tolerance to disease, increased tolerance to consider to consider tolerance to conditions, increased tolerance to disease, increased tolerance to consider tolerance to considerate, increased sensitivity to ABA, reduced sensitivity to ABA, conceased sensitivity to ABA, tolered determinacy increased tolerance attered disease, increased tolerance to conditions, altered determinacy altered determinacy altered determinacy altered sensitivity altered sensitivity altered sensitivity altered sensitivity altered send tolerance and mass, light green leaves, change in leaf shape, increased leaf fatty acide plants, dark green leaves, change in leaf shape, increased leaf size and mass, light content, altered seed coloration, altered seed side abedieved benefit altered seed coloration, altered seed side and mass, latered seed coloration, altered seed shape, increased leaf fatty acide altered seed coloration, altered seed subcontent, altered seed color
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTGACCCGGATAAAGATAGGAAGAAGGAGAAGGCTGCGGCACCGGATCACCGGTTG 213
                                                                   New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCTGGCAAGAAGAAAAAGAGGGGGGTCAACGGGGCTGTTGGACCTGATAAGAGTGGAAG
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                                                                                                                                                                                                                        present invention relates to novel plant transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 1443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1443 BP; 419 A; 273 C; 343 G; 403 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.5%; Score 157.6; DB 12; Length 56.1%; Pred. No. 6.8e-22; ive 0; Mismatches 254; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                         Claim 1; SEQ ID NO 1319; 510pp; English
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nes 348; Conservative
                    WPI; 2004-330163/30
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The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (MD061534-AD06373PB). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to cond,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant polynuclectide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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Sherman Bl
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Keddie JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1551; 510pp; English
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V, Dubell AN,
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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P-PSDB; ADO63085
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AGGICTCCCCCAATITAGIATGAAAGIGIGIGAGAAGGIAGAAAAAGCAGGGGAAGAACAC 376
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Low phosphate conduttons, increased tolerance to disease, including fungal disease and particularly Erysiphe, Fusarium and Botrytis, concreased tolerance to multiple fungal pathogens, increased resistance to increased sensitivity to ABA, reduced sensitivity to ABA, concreased sensitivity altered acabon/nitrogen sensing, early flowering, latered carbon/nitrogen sensing, early flowering, latered shoot meristem development, altered branching pattern, altered sens morphology, altered vaccular tissue structure, reduced apical dominance, altered trichome development, altered sensition, altered seed development, altered seed trichome structure, altered seed development, altered seed seed call proliferation, altered seed call proliferation, altered cell expansion, altered based call called sensition, slow growth, fast growth, altered cell differentiation, altered seed development, altered seed call proliferation, altered cell expansion, altered plants, increased caltered sensecence, abnormal embryo development, altered programmed cell feath, lethality when overexpressed, altered necrosis patterns, increased plants, darked seed coloration, altered seed size and mass, light green leaves, change in leaf shape, increased leaf fatty acids, altered seed coloration, altered seed size, altered seed coloration, altered seed seed coloration, altered seed seed size, altered seed seed coloration, altered seed seed coloration, altered seed seed size, altered seed coloration, altered seed seed coloration, altered seed seed coloration, altered seed seed coloration, altered seed protein content, altered seed seed coloration, altered seed seed coloration, altered seed coloration, altered seed seed coloration, altered seed seed coloration and seed shape, leaves, change in leaf seed shape, leav
increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low mitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to
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Length 1267; Sequence 1267 BP; 420 A; 225 C; 267 G; 355 T; 0 U; 0 Other; Pred. No. 2e-21; 0; Mismatches 258; Indels Score 155.2; DB 12; 55.78; Best Local Similarity 55.7 Matches 351; Conservative Query Match

131 AATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAAGGAAGAAGAAGGAGGAGGCT 190 418 GTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG 310 311 AAGTCCAT------GGCACATATTGGTCAAGGGTTTGATGAAGAAT 352 419 GCCACAÁTTAAGCAAAACGCAGAGAGACCTTTGAATGAAAATGAGTACAÁTGAGAÁGAAC 478 353 ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA 412 538 532 GAAATCGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAA---ACACTG 589 539 GATAAAAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGAA 598 GTCAAGATGGATCGTAATAAAGTTATGAGCAGTGTGCAAAAGAAGGCTGCTTTTCTTAAA 658 GAGTTGAGAGAAAAGGTCTCAAGTCTTGAGAGTCTTATGTCGAGAAATCAAGAGATGGTT 718 590 GAAAGCTCAGCAGAGAATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCT 649 719 Grgangacrca de de consegue de la contra dela contra de la contra de la contra de la contra de la contra dela contra de la contra del la contra de la contra de la contra del la contra d 239 ACTCCAGTGAGAAGGAATTGATTGTTGATGATTCTGAAATTGGGTCAGAGAAA GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG 359 TTGGAAGCCAAGAAGATAACTACTTACAAGGAGGTTGCAGACGAAATTATTTCAGATTTT 479 ATAAGGCGGAGAGTCTACGATGCGCTCAATGTTCATGGCGTTGGATATTATTGCAAGG CTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAG Gaps 21; 299 251 191 473 599 533 413 g ð ò g ò ద ò 요 ò 유 δ 셤 ò 셤 ò 셤 ð

779 CCTCACGCAGTAGTCGAAATCGAGATTTCTGAAGATATGCAACTTGTACACCTCGACTTC 838 Plant; transcription factor; transgenic plant; abiotic stress tolerance; somecite stress tolerance; and tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds. New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant. 650 AGGAAAGCAAGGTGGAAATTGAGATTTCAGATGACTCGAAGTTTGCCCCATTTCGAGTTC Reuber TL; Adam LJ, Re Sherman BK; Transcription factor G2981 coding sequence, SEQ ID 611. Creelman RA, Keddie JS, AATAGCACACCTTTCTCGGTCCATGATGAT 868 710 AATGGTGCACCATTCACATTGCATGAT Claim 1; SEQ ID NO 611; 510pp; English. Ratcliffe O, C V, Dubell AN, (MEND-) MENDEL BIOTECHNOLOGY INC. ADO62144 standard; DNA; 1267 18-SEP-2002; 2002US-0411837P. 17-DEC-2002; 2002US-0434166P. 24-APR-2003; 2003US-0465809P. 18-SEP-2003; 2003WO-US030292 15-JUL-2004 (first entry) Heard JE, R Arabidopsis thaliana. 2004-330163/30. P-PSDB; ADO62145. WO2004031349-A2. Riechmann JL, 15-APR-2004 ADO62144; ບັ Jiang RESULT 원 ò 셤

fungal disease and particularly Erysiphe, Fusarium and Botrytis, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ACC altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, early flowering, late flowering, altered flower structure, loss of flowering, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered trichome density, altered trichome development, altered avelopment, altered shade avoidance, altered seed development, altered seed development, altered seed germination, slow growth, fast growth, altered cell differentiation, The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold, increased germination in cold, increased tolerance to hear, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to

Arabidopsis cDNA encoding partial cell cycle protein CCP16.

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altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased blomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed protein content, altered seed protein content, increased anthocyanin levels. Note and decreased anthocyanin levels. Note The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 AATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGAAAGGCT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 155.2; DB 12; Length 1267; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1267 BP; 420 A; 225 C; 267 G; 355 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.7%;
Matches 351; Conservative (
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The invention relates to a novel cell cycle protein (CCP) and the polymuclectides encoding them. CCP is useful for identifying a compound which modulates the activity of the polympetide and which binds to the polympetide and an anti-CCP antibody is useful for detecting the presence of CCD in a sample. A CCP andilator is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP uncleic acid and polympetide molecules are useful as medulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polympetide are useful as herbicides or plant growth regulators. The colympetide are useful for modifying cell fate, plant development, plant morphology, biochemistry and/or physiology, the length of the Gl, colympetide are useful for modifying cell fate, plant development, colympetide are useful for modifying cell fate, plant development, colympetide are useful division, bNA replication, promotion, stimulation or enhancement of cell division, bNA replication, promotion, colympetide are useful and protein involved in the cell cycle due to initiation and/or development, under fruit, leaf formation, dwarfism in plants, sended size, seed development, tuber, fruit, leaf formation, and rock and the anti-CCP antibody are useful in agriculture to modulate the protein lavels or activity of a protein involved in the cell cycle due to convironmental conditions, including abiotic stress such as cold, mutrient compiration, heat, drought, salt stress, or biotic stress such as pathogen attack, to modulate e.g. enhance cells, storage tissues and/or development, endoreduplication in storage cells is useful as an immunogen to convirting CCP substrates. The polyvucle is useful for servensising CCP promition or convirting CC 86 ACTCCAGTGAGGAAATTCATTGTTGATGATGATTCTGAAATTGGATCAGAGAAA 145 screen for naturally is useful for expressing CCP cycle protein; CCP; ss; cell cycle regulation; herbicide; : growth regulator; plant development; abiotic stress; biotic stress; occurring CCP substrates. The polynuclectide is useful for expressing CCI protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence encodes a CCP protein of the New cell cycle protein and nucleic acid molecule encoding it useful fregulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators. 21; Gaps Length 1114; Sequence 1114 BP; 378 A; 197 C; 243 G; 296 T; 0 U; 0 Other; De Veylder L, Acosta JAT, Magyar Z; Indels plant growth regulator; plant development; abiotic nutrient deprivation; pathogen attack; crop yield Score 153.6; DB 6; Pred. No. 4e-21; 0; Mismatches 259; The polynucleotide Claim 38; Fig 16; 316pp; English. 14-MAY-2001; 2001WO-IB001307. (2-MAY-2000; 2000US-0204045P. Query Match
Best Local Similarity 55.6%;
Matches 350; Conservative (CROP-) CROPDESIGN NV. Arabidopsis thaliana. WPI; 2002-062249/08. P-PSDB; AAU72497. Boudolf V, WO200185946-A2 15-NOV-2001. nvention Inze D, ò 엄

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AAS96287 standard; cDNA; 1114 BP.

(first entry)

26-FEB-2002 AAS96287;

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                                                                                                                                        266 GCCACAATTAAGCAAAACGCAGAGAAGCCTTTGAATGAAAATGAGTACAATGAGAAGAAC 325
                                                                                                                                                                                             Araaggcggagagrcracgargcgcrcaargrgrrcarggcgrrggararrarggagg 385
                                                                                                                                                                                                                                                                                                                                                                      GAGTTGAGAGAAAGGTCTCAAGTCTTGAGAGTCTTATGTCGAGAATCAAGAGATGGTT 565
                                                                                                                                                                                                                                                                                                                                                                                                  590 GAAAGCTCAGCAGAGAATGTTAATGGCATCCGCTTCCATTCGTATTGGTCAAGACATCT 649
                                                                                                                                                                                                                                                                                                                                                                                                                             685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ycle protein; CCP; ss; cell cycle regulation; herbicide;
growth regulator; plant development; abiotic stress; biotic stress;
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GCGCCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA
                                                                                                                                                                   ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA
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                         GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG
                                                      GTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG
                                                                                206 TIGGAAGCCAAGAAGAIAACTACTIACAAGGAGGIIGCAGACGAAATIAITICAGAITIT
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                                                                                                                                                                                                                                                       GATAAAAAGGAAATCCCGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGAA
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                                                                                                                                                                                                                                                                                                                                            GAAATCGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAA---ACACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nutrient deprivation; pathogen attack; crop yield.
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                                                                                                            311 AAGTCCAT---
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P-PSDB; AAU72529.
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The invention relates to a novel cell cycle protein (CCP) and the polymoclectides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell of cycle or growth of a plant such as Arabidopsis thalians, rice, wheat, complete acts and cancia. CCP maize, tomato, alfalfa, oilseed rape, soybean, sunflower and cancia. CCP micles acts and cancia. CCP micles acts are production of CCP protein forms which have decreased or regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or aberrant activity. Compounds that bind to mandiate the activity of CCP protein forms which have decreased or polymoclectide are useful as herbicides or plant growth regulators. The polymoclectide is useful for modifying cell fate, plant development, of plant morphology, biochemistry and/or physiology, the length of the Gi, cplympeptide are useful as herbicides or plant, promotion, seed set.

S, G2 and/or M phase of the cell givision, DNA replication, shoot and root initiation and/or development, tuber, fruit, leaf formation, shoot and root initiation and/or development, module function, dwarfinm in plants, seed size, seed development, module function, dwarfinm in plants, some the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the coll, nutrient deprivation, heat, drought, salt stress, or biotic stress such as cold, mutrient deprivation, heat, drought, salt stress, or biotic stress such as cold development, endoceduplication in storage cells, storage tells, st New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators. Length 1189; Sequence 1189 BP; 400 A; 202 C; 260 G; 327 T; 0 U; 0 Other; Score 153.6; DB 6; Pred. No. 4.1e-21; 0; Mismatches 259; Claim 38; Fig 16; 316pp; English. Query Match
Best Local Similarity 55.6%;
Matches 350; Conservative nvention 

250 161 ACTCCAGTGAGAAGGAAATTGATTGTTGATGATGATTCTGAAATTGGATCAGAGAAAA 220 221 GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG 280 251 GTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG 310 281 TTGGAAGCCAAGAAGATAACTACTACAAGGAGGTTGCAGACGAAATTATTTCAGATTT 340 311 AAGTCCAT------GGCACATATTGGTCAAGGGTTTGATGAAAAT 352 341 GCCACAATTAAGCAAAACGCAGAGAGCCTTTGAATGAAAATGAGTACAATGAGAAGAAC 400 353 ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA 412 GAAAAAAAAGGAGATACGGTGGATGGGCCTTTCAAATTACAGATATGAAAATAAAGAAG 472 131 AATGCGGTCCAAAGGAAGGGCGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGGAGAAGGTT 191 GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA 413 요 셤 g ò 셤 g ò ઠે ò ઠે

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521 GTCAAGATGGATCGTAATAAAGTTATGAGCAGTGTGCQAAAAGAAGGCTGCTTTTCTTAAA 580

473 CTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAG 461 GATAAAAAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGAA

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Gaps

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Length 1274;

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                                                                                                                                 246 ACTCCAGTGAGAGGAAATTGATTGTTGATGATTCTGAAATTGGATCAGAAGAAA
                                                                                                                                                                                                                                                                     251 GTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG
                                                                                       AATGCGGTCCAAAGGAAAGGAGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                              ---GGCACATATTGGTCAAGGGTTTGATGAGAAT
                                                                                                                                                                                GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA
                                                                                                                                                                                                                                                                                                                  366 Triggaagccaagaagaraacracracaagaagarigcagacgaaarrarricagarrir
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    DB 10;
Score 153.6; DB 10;
Pred. No. 4.2e-21;
0; Mismatches 259;
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/product= "DP protein"
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  atch 14.1%;
al Similarity 55.6%;
350; Conservative
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       Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E2F
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                                                      GAGTTGAGAGAAAGGTCTCAAGTCTTGAGAGTCTTATGTCGAGAATCAAGAGAGATGGTT 640
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members of the plant
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              GAAATCGAAAAACAGTTTGATGATCTCCCAAAACATCAAGTTACGTAACCAA---ACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Broekaert W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene therapy; stress resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modifying cell number, architecture and yield of modulating the expression and/or the activity of transcription factor family.
                                                                                                         GAAAGCTCAGCAGAGAATGTTAATGGCATCCGCCTTCCA
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                                                                                                                                                                                                                                                                                   710 AATGGTGCACCATTCACATTGCATGAT 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Dillen W, Frankard V;
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27-MAR-2003

Dillen W,

(CROP-)

25-MAR-2004

ADH59559

761

RESULT 12 ADH59559 845

06-MAR-2003

Sequence 1274 BP; 420 A; 228 C; 271 G; 355 T; 0 U; 0 Other;

589

725

545

310 425 352 605 532 665

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in a plant, or a part of the plant. The method comprises modifying the expression or activity of an E2F and DP gene or polypeptide. Also described: (1) a transgenic plant cell overspressing an E2F or E2F agene, or an E2F and DP gene or an E2F and DP gene, or an E2F or E2F agene, or an E2F and DP gene or the DP or DP gene is under the control of a tissue or cell-type specific promoter: (2) a transgenic plant, or a part of the plant comprising the cells described above; (3) a progeny of the plant described above; and (4) a plant material obtained from the plant described above; TF method is useful in modilating plant cell cycle proteins by modifying the expression or activity of an E2F and DP gene or polypeptide. The present sequence encodes Arabidopsis thaliana DP, which
                                                                                                                                                                                                                                                  Modulating endoreduplication in a plant, or a part of the plant, comprises modifying the expression or activity of an E2Fa and DPa gene or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAATCGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAA---ACACTG 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for modulating endoreduplication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GGCACATATTGGTCAAGGGTTTGATGAGAAGAAT 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486 ATAAGGCGGAGAGTCTACGATGCGCTCAATGTGTTCATGGCTTGGATATTATTGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGGAGAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 GITGAAGCCAAAGGAAGAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 1274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1274 BP; 420 A; 228 C; 271 G; 355 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 153.6; DB 10; Length
Pred. No. 4.2e-21;
0; Mismatches 259; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used in the exemplification of the present invention
                                                                                                                                                Mironov V, Segers G;
                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 25-26; 34pp; English.
                     26-AUG-2002; 2002WO-EP009504.
                                                             24-AUG-2001; 2001US-00938342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.6%;
Matches 350; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 AAGTCCAT-----
                                                                                                                                             De Veylder L, Inze D,
                                                                                                      (CROP-) CROPDESIGN NV.
                                                                                                                                                                                       WPI; 2003-300735/29.
                                                                                                                                                                                                           P-PSDB; ABP96848
                                                                                                                                                                                                                                                                                           polypeptide
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The present invention relates to novel plant transcription factor

proteins (1) and nucleotide sequences (11) (ADO61534-ADO63778). The

sequences can be used to produce transgenic plants, which overexpress

(II), where the transgenic plant has an altered trait as compared to a

non-transgenic plant or wild-type plant. The transgenic plant comprises

con-transgenic plant or wild-type plant. The transgenic plant comprises

con-transgenic plant or wild-type plant. The transgenic plant comprises

con-transgenic plant or wild-type plant. The transgenic plant comprises

con-transgenic plant or wild-type plant. The transgenic plant comprises

con-transgenic plant or wild-type plant. The transgenic plant comprises

con-transgenic plant or wild-type plant. The transgenic plant comprises

con-transgenic plant or wild-type plant. The transgenic plant conditions, increased tolerance to low introgen conditions, increased tolerance to low introgen conditions, increased tolerance to comprise the plant pathogens, increased tolerance to comprise the plant p
                                    786 CCTCACGCAGTAGTCGAAATCGAGATTTCTGAAGATATGCAACTTGTACACCTCGACTTC 845
709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant; transcription factor; transgenic plant; abiotic stress tolerance; sendic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
650 AGGAAAGCAAGGGTGGAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTC
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Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cliffe O, Creelman RA,
Dubell AN, Keddie JS,
                                                                                                                                      846 AATAGCACCTTTCTCGGTCCATGATGAT 875
                                                                                                 710 AATGGTGCACCATTCACATTGCATGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2093; 510pp; English.
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Haake V, Dubell A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                             ADO63626 standard; DNA; 1153
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-2003; 2003WO-US030292
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2004
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altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell ceath, lethality when overexpressed, altered necrosis patterns, increased plant size, increased blomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large eed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed protein content, increased anthocyanin levels, and altered leaf prenyl lipid content, increased anthocyanin levels, and not form mattof the printed specification, but was obtained in clectronic format directly from WIPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 ATCAGAAACAATATGATGAGAAGAACATCAGACGACGACGAGTCTAGGATGCTCTGAACGTAC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTACAGATATGAAAAATAAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACTGATGCAAATGATATTGAGGAGCTAAAGACTGAGCGTCTTAACTTGAGAAATAGGA 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1153 BP; 337 A; 225 C; 267 G; 324 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  14.1%; Score 153.4; DB 12; Length 55.1%; Pred. No. 4.5e-21; ive 0; Mismatches 271; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAATCCTTGAGGGGGTAAGGCGTAACAGCATAGGAAGAGCTGG 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 55.1
hes 354; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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AAFB0146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a heterodimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly organ or tissue size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                   factor; G1 phase;
proliferation;
                                                                                                                                                                                                                                                                                                                                                                                       New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAAAAGGAAGAACAACATACAATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 GATAAAGATAGGAAGAAGGAGGAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
     DNA fragment encoding a wheat E2F-dimerisation partner (DF) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                    F-dimerisation partner; DP protein; E2F transcription phase; cell cycle; retinoblastoma protein; alter cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 153 BP; 55 A; 25 C; 47 G; 26 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                               (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match
Local Similarity 100.0%; Pred. No. 3.6e-21;
hes 153; Conservative 0; Mismatches 0;
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                                             E2F-dimerisation partner;
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11-JUN-2001 (first entry)

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CD892664 G118.121J
EB456002 HVSMEGO1
CR289243 CR289243
CL959517 OGIFCC003
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9755.705 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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/culfivar="recital" /db_xref="taxon:4565" /db_xref="taxon:4565" /clone="Filling2" /clone_Tib="leaf one" /clone_Tib="FI" /clone_Tib="FI" /clone_Tib="filling one" /clone_Tib="filling one" /clone_Tib="filling one" /city 96.4%; Score 614.4; DB 6; Length 649; /city 96.4%; Pred. No. 1.8e-123; Indels 0; Gaps 0	Simila: 7; Col	ORIGIN Query Match Best Local Matches 62
Genoplante  33. rue Henri Rochefort 91025 EVRY CEDEX France  13. rue Henri Rochefort 91025 EVRY CEDEX France  13. 1 69 47 54 10  This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).  Location/Qualifiers  1. 649    cognime=Triticum aestivum"   mol type="recital"   cultivar="recital"   cultivar="recital"   cultivar="recital"   cultivar="recital"   cultivar="recital"   cultivar="recital"	Genoplar 93, rue 791, rue 791, rue 7 Fax: 33 This se plant g	FEATURES
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum. The (bases 1 to 649) Genoplante. Genoplante, a major partnership french program in plant genomics Unpublished (2003)	Spermatophyta; Magn Pooideae; Triticeae I (bases I to 649) Genoplante. Genoplante, a major Unpublished (2003)	REFERENCE AUTHORS TITLE JOURNAL COMMENT
:32645392 vum (bread wheat)	seguence. CD882927 CD882927.1 GI:32645392 EST. Triticum aestivum (bread wheat) Triticum aestivum	ACCESSION VERSION KEYWORDS SOURCE ORGANISM
ALIGNMENTS 649 bp mRNA linear EST 14-JUL-200 r1 Triticum aeetivum cDNA clone F1111L02, mRNA	CD882927 F1.11102F010430	RESULT 1 CD882927 LOCUS DEFINITION
CK754643 CK919899 CD813391	111 10.2 5 0.6 10.2 6 110 10.1 7	11
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62 AATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATGGCACTTCGTGTTATGGCA

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Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Dec 2, 2002 this sequence version replaced gi:25994251 Contact: Richard Bruskiewich Biometrics and Bioinformatics Unit International Rice Research Institute DAPO 777, Metro Manila, Philippines
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International Rice Information System (IRIS;
International Rice Information System (IRIS;
Assignment of putative function to the sequence |
Munich Information Center for Protein Sequences (http://mips.gsf.de)
Inter:/mips.gsf.de)
Location/Qualifiers
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Brusktenich, R.M.
IRRI Drought Stress Panicle cDNA Library
Unpublished (2002)
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/organism="Oryza sativa (indica cultivar-group)"

mol type="mRNA"

cultivar="IRRA"

/db xref="taxon:39946"

/clone="C0001827"

/tissue type="Panicles"

/dev_stage="Plowering"

/dev_stage="TRNE Drought Stress Panicle Library"

/clone lib="IRRI Drought Stress Panicles applied by not watering for 4 consecutive days. Panicles applied by not watering for 4 consecutive days. Panicles were collected from control (well watered) and stressed plants at 2 days before heading, at heading, 50% flowering and 4 days after 50% flowering."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCAGAGAATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              cch 38.7%; Score 421.6; DB 6; al Similarity 77.1%; Pred. No. 2.2e-81; 581; Conservative 0; Mismatches 153;
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CD892664 121J23F010725 G118 Triticum aestivum cDNA clone G118121J23,
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                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticeae; Triticum.
(Dases 1 to 454)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCGCCACCCTTCACTAGAGACTCAAGAATATTACAAATGAATTAAAAAGTTGTCAGAACT 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 TTTGTGCCTAGCAGGTTATTAGGTCCAAGATAGATGATTCGTATATGTGCTGCTATGTA 430
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                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr)
                                                                                                                                                                                                                                                                            Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCGCCACCCTTCACTAGAGCTCAAGAATATTACAAATGAATTAAAAAG-TGTTAGAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="grain (118 degrees per day after
pollination)"
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                                                                                                                                                                                                                                                                                                                                                       93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Triticum aestivum"
                                                                                                                                     Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4565"
/clone="G118121J23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="recital"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="G118"
                                                                                             CD892664.1 GI:32663198
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Genoplante
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Hordeum vulgare subsp. vulgare

Bukaryora, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;

Bukaryora, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

Is (bases 1 to 607)

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D.,

Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W.,

Fenton, R.D., Close, S.J., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource for barley genomics Morex pre-anthesis spike cDNA library

Unpublished (2001)

On Jul 26, 2000 this sequence version replaced gi:13155022.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University
                                  BE456002 607 bp mRNA linear EST 22-OCT-2001
HVSNRS90199117f Hordeum vulgare pre-anthesis spike EST library
HVCDNAA0008 (white to yellow anther) Hordeum vulgare subsp. vulgare
CDNA clone HVSMEG0019D17f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total hq bases = 141
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 585.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                              BE456002.3 GI:16318905
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Query Match

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Oryza sativa

Oryza sativa

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhatroideae; Oryzae; Oryza

1 (bases 1 to 612)

1 (bases 1 to 612)

2 han, B., Feng, O., Huang, Y. C., Ying, K., Li, Y., Guan, J. P., Zhu, J. J.,

Zhao, O., Hu.X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L.,

Weng, O.J., Zhang, L., Lu, Y. Q., Yu, S. L., Liu, X. H., Lu, T. T.,

Zhang, Y. J., Lu, Y., Li, C., Li, T., Zhang, Y., Hu, H., Jia, P. X.,

Zhang, L., Lan, L. F., Chen, W., Mu, S. A. and Xue, Y. B.
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                                                                                                            ACCTGACCGGCGTGCACATTCTCGAAGCTTCCAGTGTCCCCCCCGCTTCCCGAA---GCGG 125
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                                                                                                                                                                          GCGGTAATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGA 185
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                                                                                                                                                                                                                                                              AGGCTGCGGCACATAGGATCACCGGTTGGGGGCTCCGCGAATACAGCAAAATAGTTTGTG 267
                                                                                                                                                                                                                                                                                                      AGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAG 305
                                                                                                                                                                                                                                                                                                                                    AGAAAGTTGAAGCCAAAGGAAGAACATCATACACTGAGGTTGCGGATGAAAATTATTCAG 327
                                                                                                                                                                                                                                                                                                                                                                   AGCTGAAGTCCATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAG 365
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                                                             28 CTCGAACCGCAATGGCGCCTCCCCGCGGAGGTGCTGCTGCGGGCCGTTCCCGCCGCACTGG
                                                                                                                             CACGAGCCGCAATGGCGCCTCCCCGCGGCGGAGCTGCTGCGGCCGCTACCGCCGCACTGG
                Gaps
               7;
Pred. No. 1.5e-71;
0; Mismatches 56; Indels
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Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 200233,
Email: bhan@ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa"
/mol_type="mRNA"
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This is rice cdna est clone
Web site: http://www.ncgr.ac.cn.
Location/Qualifiers
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87.9%;
                457; Conservative
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Matches 45
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OSIFCC003026 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                      AAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACT
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                                                                                                                                                                                                              TGCAAAAAAAAAAAAAGGAGATACGGTGGATGGGCCTTTCAAATTACAGATATGAAAAAT
                                                                                                                                   GTACAGCAAAATAGTTTGTGAAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGT
                                                                                                                                                               1 GTTCAGCAAGATAGTTTCTAAGAAAGTTGAGGCCAAAGGAAGAACCACATATAATGAGGT
                                                                                                                                                                                                                                                        GAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTAT
                                                                                                       Gaps
                                                                                                       ö
                                                                          612;
                                                                        Length
/db_xref="taxon:4530"
/clone="p704a10p5"
/clone_lib="Oryza sativa library (Han B)
                                                                                                       Indels
                                                                       Score 373.8; DB 7;
Pred. No. 5.7e-71;
0; Mismatches 112;
                                                                          Query Match
Best Local Similarity 79.7%;
Matches 441; Conservative
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                    REFERENCE
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547
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                                                                                                                                                                      /organism="Oryza sativa (indica cultivar-group)"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic py46"
/clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                            33.8%; Score 368.2; DB 9; Length 1119; 78.8%; Pred. No. 1e-69; ive 0; Mismatches 118; Indels 0;
Chinese Academy of Sciences, Beijing 101300, China
                                                           Email: chenchen@genomics.org.cn
                                                                                                    Class: exon-trapped.
Location/Qualifiers
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                                                                                    Rice genomic sequence.
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Saccharum officinarum
                    Tel: 86-10-80481559
Fax: 86-10-80488676
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 78.8
Matches 439; Conservative
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/lab host="DHIOB"
/clone lib="AM1"
/clone lib yetcor: pSport1; Site 1: Sal1; Site 2:
/clone lib yetcor: pSport1; Site 1: Sal1; Site 2:
/clone lib yetcor: pSport1; Site 1: Sal1; Site 2:
/clone lib were from library generated from library construction can be and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                                                                                                                         Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 1010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found http://www.bcccenter.fcav.unesp.br
http://www.bcccenter.fcav.unesp.br
Plate: 006 row: A column: 02
Seq primer: T? Promoter Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 GAGGTTGCAGATGAAATTTGTGGGGAGCTGAAG---CTGACTCTTATTGGTCAAGAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 GATGAGAAGAATATTAGGCGGAGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 GTTATTGCAAAAGAAAAAAGGAGATACGGTGGATGGGCCTTTCAAATTACAGATATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 GITATTACAAAAGACCAAAAGGAGATAAAGTGGATGGGCTTGTCTAACTTCCAATATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 AAAATAAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 CCGGATAAAGATAGGAAGAAGGAGAAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                            and Arruda, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Saccharum officinarum"
                                                  Kemper, E.L.
                           Vettore, A.L., da Silva, P.R., Kemper, E.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="SCRLAM1006A02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:4547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
(bases 1 to 665)
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403 374

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ENKAYORA, VITIGIPALATES, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

2E (bases 1 to 634)

3S Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Eastman, A. and Pratt, L.H.

An EST database from Sorghum: pollen
Unpublished (2003)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sorghum bicolor"
/mol type="mRNA"
/cultivar="mRNA"
/cultivar="mRNA"
/cultivar="mRNA"
/cultivar="mRNA"
/cultivar="mran:4558"
/clone="poil 25 C08 A002"
/lab host="pHi0B-TI phage-resistant E. coli"
/lab host="pHi0B-TI phage-resistant E. coli"
/clone lib="Pollen"
/clone lib="Pollen"
/note="Organ: Pollen"
/note="Organ: Pollen"
/site 1: XhoI;
/site 1: XhoI;
/site 2: XhoI; The labrary was prepared from polyA+ RNA
from pollen at the late vacuolated-vacuolated stage of
development. Pollen was harvested from greenhouse-grown
panicles of sorghum line BTx623. Panicles were removed
from the flag leaf prior to emergence, when no detectable
amylase is present in pollen of male-fertile lines. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 08-SEP-2003
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Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genter, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A. & M University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 ATTGCAAAAGAAAAAAGGAGATACGGTGGATGGGCCTTTCAAATTACAGATATGAAAAA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 ATABAGAAGCTTGAAGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 ATA---AAGTIGGAGGAAACTCGAAAGAACTCATGATCAGGATTAAGAACAAGAAAAA 491
198 GAGTICAGCAAGATAGTITCTAAAAAGGTTGAGACCAAAGGACGGACTACTTACAGTGAG 257
                                                                                                   GTTGCAGACGAAATTTATTCAGAGCTGAAGTCCATGGCACATATTGGTCAAGGGTTTGAT
                                                                                                                                                                                             258 GTTGCAGATGAAATTTGTGGAGAGAGT----TGACTCTTATTGGTCAAGAGTTTGAT
                                                                                                                                                                                                                                                                                       344 GAGAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTT
                                                                                                                                                                                                                                                                                                                                              315 GAGAAGAATATCAGGAGAGAGAGTGTATAGATGCTTTTAATGTGCTAATTGCACTACGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524 CTCCTCCAGGAAATCGAAAACAGTTTGATGATCATCCAAAACATCAAGTTACGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 CTTCTCCAGGAAATTGAAAGACAGCTTGATGACCTCCAGAATATCAAGTTTCGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          634 bp mRNA linear Ek
POLI 25_C08.91_A002 Pollen Sorghum bicolor cDNA clone
POLI 25_C08_A002 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: Sugs (CTTCTGCTCTAAAAGCTGCG)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF484481.1 GI:34513350
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CF484481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE511883 548 bp mRNA linear EST 07-AUG-2000 946064A10.yl 946 - tassel primordium prepared by Schmidt lab Zea mays CDNA, mRNA sequence. BE511883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: tassels, Vector: HybriZAP; Site_1: EcoRI; site_2: KhOi, George Chuck dissected immature tassels between Imm and 3mm. Sharon Stanfield prepared the CDNA library in HybriZAP. Sample insert size range was 350 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAAAGGAAGAAGAAGAACATACAATGAG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crircicio de accesa de concesciones de contra 
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                                                      521 GCACTCCTCCAGGAAATCGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAAC 580
                                                                                                                                                561 AAACTICICCAGAAATICAACGACAGGITGAIGACCITCAGAATAICAAGTICCGCAAC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 548)
Walbot,V.
Malbot,V.
Malsot,V.
Malsot,V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
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lab"
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Fax: 650 725 8227
Email: walbot@stanford.edu
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1 (bases 1 to 702)
Han, B., Feng, Q., Huang, Y.C., Ying, K., Li, Y., Guan, J.P., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Zhao, Q., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, T., Zhang, Y., Hu, H., Jia, P.X., Zhang, L., Lan, L. E., Zhang, L., Lan, L. E., Chen, W., Wu, S.A. and Xue, Y.B.
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stage represents pollen collected from anthers about 8-1 days prior to anthesis. Double-stranded CDNA was cloned unidirectionally into different DraIII sites of the PMENSF-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the CDNA insert."
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CR268682 Oryza sativa library (Han B) Oryza sativa cDNA clone
CR286882 CR286882
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9
                                                                                                                                        Score 264.2; DB 7; Length 634;
Pred. No. 4.7e-47;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 TGATGACCTTCAGAATATTACATTAAGCAAACCAGGCTAGTACGAGGCCAGGACAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           609 TTAATGGCATCC--GCCTTCCATTCGTATTGGTCAAGACA--TCTAGGAAAGCAAGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                                                                                                                                                                                                                                                                                                                                                                               702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 CGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGGTACAGCAAAATAGT
                                                                                                                                                                                                                                                                                                                                                      (Han B) "
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                          1. .702,
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="p730d01p5"
/clone_lib="Oryza sativa library
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 237.8; DB 7;
Pred. No. 2.7e-41;
0; Mismatches 112;
                                                                             China
Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 200233, CP
Email: bhan@ncgr.ac.cn
Clone requests: bhan@ncgr.ac.cn
This is rice cdna est clone
Web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI802607
BI802607.1 GI:16575311
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75.7%;
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373; Conservative
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OA ABa0009114.f OA ABa Oryza australiensis genomic clone
OA ABa0009114 5', genomic survey sequence.
                                          CL<u>9</u>09692
CL909692.1 GI:52018571
GSS.
                                                                                                          Oryza australiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 74.8
Matches 246; Conservative
                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                               TITLE
JOURNAL
COMMENT
  DEFINITION
                                                                                                                                                                                                                REFERENCE
AUTHORS
                                            ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                614 GGCATCCGCCTTCC-ATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGTGGAAATTGA 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     673 GATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTCAATGGTGCACCATTCACATTGCA 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGATGATCTCTCAATCCTTGAGGGGGTAAGGCGTAACAGCATAGGAAGAGCTGGCCGCGC 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACAGCCGGATTCTTTTGCACAGCTATGTATAGCTATA-----TATCCTCATGAAA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 GCACCACCAGTTTCTTTTGCACAGTTATGTATAGCTATAGCGTACCTTTCAGTATGGAAA 359
                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Endosperm"
/dev_stage="10 days after anthesis"
/clone_lib="Endosperm library from Oryza sativa (10 days
after_anthesis)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACCTTCCAGAATATACATTACGCAACCAGGCTAGTCAGAGGCCA-CAGAAAGTGTTAAT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 TGATGATGTATCAATCCTTGAAGCCATCAGGCGTAACAACAACAAAGAAGGAGCTGGCCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              554 GATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAGAATGTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCCTTCACT-AGAGACTCAAGAATATTACAAATGAATTAAAAGTG----TTAGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 TTATGTATAAACTCATTGCCGTTTCAATTCGAAGCTTGTGTACAAGCTCCATTGATGAAA
  Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                              Email: webmaster@estarray.org, URL: http://www.estarray.org
Seq primer: M13 forward primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 218; DB 4; Length 548;
Pred. No. 5.6e-37;
0; Mismatches 140; Indels
                                                                                                                                Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
                                                                                      Contact: Haitao Dong, Debao Li
Bioinfomatics and Gene Network Research Group
                                                                                                                                                                                                                                                                               1. .548
/organism="Oryza sativa"
/mol_type="mxNA"
/db xref="taxon:4530"
/clone="H084D10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Vector: pSport2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.0%;
Best Local Similarity 71.1%;
Matches 391; Conservative
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CL909692/c
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CK278661 BST724739 potato abiotic stress cDNA library Solanum tuberosum cDNA
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| Tab hogt="DHIOB TI phage resistant"
|/clone lib="OA ABa"
|/note="Vector:"pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 836)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 TATGACCTGCGAATTTTTGCCTCTTTTTTGTGCCTAGCAGGTGA----GTCTGGAATAGGTG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            714 GIGCACCATICACATIGCATGATGATCTCTCAATCCTTGAGGGGGTAAGGCGTAACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 GIGCACCATCACCATGCATGATGATGTCTCAATCCTTGAAGCCATCAGGCGTAACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 TAGGAAGAGCTGGCCTCTCCATTCTCCCTTAAAGAGACACAAAAATGTGACAAAAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   886 --ATAICCICAIGAAAACTIGACCIAGITTAIAGGACAGICTCICAGGCITGAGAAGAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     774 TAGGAAGAGCTGGCCGCCCCCCTTCACT--AGAGACTCAAGAATATTACAAATGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                832 AAAAGIGITAGAACIGGCACAGCCGGAIICITIIGCACAGCIAIGIAIAGCIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 836;
                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                  OMAP Project
Unpublished (2004)
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, US
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%; Score 160.6; DB 9; 74.8%; Pred. No. 1.9e-24; ive 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .836
/organism="Oryza australiensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0009 row: I column: 14
Seq primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db xref="taxon:4532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="OA_ABa0009114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CK278661
LOCUS
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228 ATCAGAAACAATATGATGAGAAGAACATCAGACGAGGTCTACGATGCTCTGAACGTAC 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="potatio abiotic stress cDNA library"
/clone lib="potatio abiotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site_1: ECORI; Site_2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a lahr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mm Nacl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 14d, 2d, and 4d; roots12hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were beat stressed by placement at 3 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed at 2 hr, 6 hr, 12 hr, 1 d,
br, 1 A and 4d and heat-stressed at 2 hr, 6 hr, 12 hr, 1 d,
br, 1 h and 4d and heat-stressed at 2 hr, 6 hr, 12 hr, 1 hr,
br, 1 h and 4d and heat-stressed tools were harvested at 6 hr,
br, 1 h and 4d and heat-stressed roots were harvested at 6 hr,
br, 1 h and 4d and heat-stressed roots were harvested at 6 hr,
br, 1 h and 4d and heat-stressed roots were harvested at 6 hr,
br, 1 h and 4d and heat-stressed roots were harvested at 6 hr,
br, 1 h and 4d and heat-stressed roots were harvested at 6 hr,
br, 1 h and 4d and solds were harvested at 8 hr, 8 hr, 12 hr, 10 hr,
br, 1 h and 4d and heat-stressed roots were harvested at 6 hr,
br, 1 h and 4d and foods were harvested at 8 hr,
br, 1 h and 4d and heat-stressed roots were harvested at 6 hr,
br, 1 h and 4d and 6d for sold stressed leaves were harvested at 6 hr,
br, 1 h and 4d and 6d for sold stressed leaves were harvested at 6 hr,
br, 1 h and 4d and 6d for sold stressed leaves were ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGGAAAAAGAAAAGAGTCAGCGTGCTACTGGAGGGGATAAAAGTGGTAGAGACTCA 107
                                                                                                                                                                           Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 AGGTTGCTGATGAACTTGTAGCTGAGTTTTCTGATGCTACCAATAGTGTTGCAGGCCCAG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheog Spermatophyta, Magnollophyta, eddicotyledons, core eudicots, asterids, lamides Solanales, Solanaceae, Solanum.

(Dases 1 to 992)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, Generation of EGTs from abiotic stressed potato tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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Pred. No. 9.9e-23;
0; Mismatches 252; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
clone POAE738 5' end, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db xref="taxon:4113"
                                                                                                                 Solanum tuberosum (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="POAE738"
                                                                                                                                                                                                                                                                                                                                              Unpublished (2003)
Other ESTS: EST724740
Contact: Robin Buell
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Best Local Similarity 55.9°
Matches 342; Conservative
                                                                                                                                             tuberosum
                                                       CK278661.1
                                                                                                                                          Solanum
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VERSION
KEYWORDS
SOURCE
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1 (bases 1 to 1403)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Craudd, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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446
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                                                                                288 TTATGGCTATGGATATCATTTCTAAAGATAAAAGGAAATACAGTGGAAGGGATTACCAC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   647
                                                                                                                                                                                                                                                    348 GCACTGATGCAAATGATATTGAGGAGCTAAAGACTGAGCGTCTTAACTTGAGAAATAGGA 407
                                                                                                                                                                                                                                                                                                                                                                                                                        408 TIGAAAAGAAAGCAGCCTATITAGAAGAACTIGAAGATCAATATGTAGGGCTICAAAACC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATAAAAACGCAATGATCAGTTGTATGGCTCAGGCAATGCTCCTAGTGGTGGTGTGGCTT 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             567 TCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAGAATGTTA---ATGGCATCCGCC 623
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Castelli
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The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length libraixies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castell V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Mancation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                                                                                                                                                                    TTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAACAGTTTGATGATCTCCCAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 TACCGTTTATTTTAGTGCAGACTCGTCCTCATGCAACAGTTGAAGTGGAAATATCAGAAG
                                                                                                                                                                447 ATTACAGATATGAAAAATAAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      684 ACTCGAAGTTTGCCCATTTCGAGTTCAATGGTGCACCATTGCATGGATGATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          588 ATATGCAGCTGCATTTCGACTTCAACAGCACTCCGTTTGAGCTACATGACGATAATT
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Arabidopsīs thaliana (thale cress)
Arabidopsīs thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo)
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/db_xref="taxon:3702"
/clone="GSLTLS81ZA03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Col-0"
                                       (bases 1 to 1418)
                                                                                                                                                            (bases 1 to 1418)
                                                                                                                                                                                           Direct Submission
                                                                                                                                               Unpublished
                                                                                                                                 Annotation
                                                                                                                                                                             Genoscope.
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone SSLTLS81ZA03 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).

BX831357
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                                                                                                                                                                                                                                                      147 AGGGGCTGTTGACCCGGATAAGATAGGAAGAAGAAGAAGGCTGCGGCACCGAGGATCA 206
                                                                                                                                                                                                                                                                                                                 CCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAAAGGAA 266
                                                                                                                                                                                                                                                                                                                                             545
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                                                                                                                                                                                                                                                                                  AAGGAGCTTCTGGTGTTAAGAAGAAGAAGAGGGGACAGCGTGCGGCTGGTCCAGATAAGA 485
                                                                                                                                                                                                                                                                                                                                                                           ---GA 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             552 ATGATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGGTCAGCAGAGAATGTTA
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                                                                                                                                                                                                                          18;
                                                                                                                                                                                           Length 1403;
                                                                                                                                                                                         Score 150.8; DB 3; Length
Pred. No. 2.8e-22;
0; Mismatches 262; Indels
                                                                                                /tissue type="Adult vegetative tissue"
/plasmid="pCMVSPORT_6"
1. .1403
                                                                                                                                                                                                                                                                                                                                                                           GAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCT-
                            organism="Arabidopsis thaliana"
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HTC; GSLT CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                    /db_xref="taxon:3702"
/clone="GSLTLS67ZA12"
ocation/Qualifiers
                                                                                                                                               /gene="At5g03415"
                                          /mol_type="mRNA"
/strain="Col-0"
                                                                                                                                                                                           Query Match
Best Local Similarity 55.3%;
Matches 346; Conservative
               .1403
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Were genoscope.coms. Interest is sequenced by the sequences are based on single pass reads.

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Manotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full
                                                                                                                                                                                                                                                   Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AGGGGGCTGTTGACCCGGATAAAATAGAAAAAAAAAGAGAAGAAGGCTGCGGCACCGAGGATCA
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Location/Qualifiers
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/plasmid="pCMVSPORT_6"
1. .1418
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    11. 1418
    /organism="Arabidopsis thaliana"

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Best Local Similarity 55.0%; Pred. No. 1e-21;
Matches 345; Conservative 0; Mismatches 2
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Search completed: February 6, 2005, 15:46:10
Job time : 4259 secs
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Sequence Seq

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Scoring table:

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ZIF: 94304

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Derfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
                                           -09-602-877A-95
-09-621-976-14761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1456
Sequence 1456
Sequence 1456, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
ITLE OF INVENTION: COMPOSITION FOR THE DE:
ITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                 US-09-182-816-22
US-09-182-816-24
                                                                                                                                                                                                                            US-09-471-528-22
US-09-471-528-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMUNICATION INFORMATION:
TELEPRONE: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1456:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2320 base pairs
                                           TYPE: nucleic acid
STRANDEDNESS: single
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; LIBRARY: GENBANK
; CLONE: g604478
US-09-023-655-1456
Query Match
Sequence 1, Appli
Sequence 1399, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 566, App
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7815.374 Million cell updates/sec
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Sequence 120497,
Sequence 120498,
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                                                                                                                                                                                                                                                                                            Seguence 3,
Seguence 3,
Seguence 3,
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Sequence 1
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-3349
US-09-189-627A-5
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US-09-640-211A-465
US-09-640-211A-465
US-09-72-345B-3
US-09-627-3415B-3
US-09-189-627A-3
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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Result

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347 AAGAATATTAGCGGGAGAGTGTATGATGCTTTTCAACGTTCTCATTGCACTTCGTGTTATT 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 GTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATT 298
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467 AAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTC 526
                                                699 cagaatcrocagatagaagcagagccggaragaacggaraaagcagaaagcgggcccag 758
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                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: detaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                     527 CICCAGGAAATCGAAAAAAGTTTGATGATCTCCAAAACAT 567
                                                                                                                                                     759 chgcaagaachrcrccracagcaaarcgchrhcaaaacch 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: J0-SEP-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: J0-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CTANGORD, ARTHUR R.
REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 117-220
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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56.0%; Pred. No. 7.6e-12;
iive 0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              Sequence 5, Application US/08723415B
Patent No. 5859199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1157 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 191; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION:
US-08-723-415B-5
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US-09-949-016-3349

i Sequence 3439, Application US/09949016

patent No. 681239

i GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOU3307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2000-09-08

SOUTHWARE PRESENCE OF WINDOWS VERSION 4.0
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                                                                                236 ATAGTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAA 295
                                                                                                                                                                                                                                                                                                                                           489 CAGAAGAACATTAGGCGAAGAGTTTATGATGCTTTAAATGTGCTAATGGCAATGAACATA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                           609 TGTCAGAATCTGGAGATAGAGAAGCAGAGGCGGATAGAACGGATAAAGCAGAAGCGGGCC 668
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                                                                                                                                369 AAAGTGTGTGAGAAGTTCAACGAAAAGGTACAACATCGTACAATGAAGTCGCTGATGAG 428
                                                                                                                                                                                     296 ATTTATTCAGAGCTG------AAGTCCATGGCACATATTGGTCAAGGGTTTGAT 343
                                                                                                                                                                                                                                      429 CTGGTGTCAGAGTTCACCAATTCAAATAACCATTTGGCTGCTGATTCGCAGGCTTATGAT 488
                                                                                                                                                                                                                                                                                        344 GAGAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 ATAAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCA 523
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                                Gaps
                                12;
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                             Indels
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Pred. No. 1.6e-14;
0; Mismatches 135; Indels
        58.1%; Pred. No. 6.8e-15; ive 0; Mismatches 132;
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Best Local Similarity 57.8
Matches 197; Conservative
                             200; Conservative
        Similarity
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ORGANISM: Human
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        Best Local
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                                                                               467 AAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGACCTC 526
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                                       364 TCAAAGGAAAAAAAGAAATCAAGTGGATTGGCCTGCCTACCAATTCTGCTCAGGAATGC 423
                                                                                                                       244 GTATCTGAGTTTACCAACTCAAATAACCATCTGGCAGCTGATTCGCAGGCTTATGATCAG 303
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                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR PLILING DATE: 1996-09-15
PRIOR PLILING DATE: 1996-05-15
SROFTWARE: PALENTIN VOY: 2.0
SEQ ID NOS: 25
SOFTWARE: PALENTIN VOY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86.2; DB 3; Length 1157;
Pred. No. 7.6e-12;
0; Mismatches 138; Indels 12;
                                                                                                                                                                   CTCCAGGAAATCGAAAACAGTTTGATGATCTCCCAAAACAT 567
                                                                                                                                                                                                           484 CTACAAGAACTICTCCTTCAGCAAATTGCTTTTAAAACCT 524
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                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09189627A Patent No. 6159691 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-710-861-5; Sequence 5, Application US/09710861; Patent No. 6387649; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 56.0°
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)..(1110)
US-09-189-627A-5
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US-09-189-627A-5
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239 GTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATT 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 GTATCTGAGTTTACCAACTCAAATAACCATCTGGCAGCTGATTCGCAGGCTTATGATCAG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 AAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407 GCAAAAGAAAAAAGGAGATACGGTGGATGGGCCTTTCAAATTACAGATATGAAAAATA 466
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APPLICANT: de la Lura, Susana;
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF;
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/180, 627
CURRENT FILING DATE: 2000-11-13
FRIOR PELICATION NUMBER: US/09/180, 627
PRIOR PELICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN UNER: 08
SOFTWARE: PATENTIN UNER: 08
SOFTWARE: PATENTIN UNER: 08
SOFTWARE: PATENTIN UNER: 08
SOFTWARE: DATENTIN UNER: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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APPLICANT: Wood, Marion
APPLICANT: Wood, Marion
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REPERENCE: 11000.1021CJU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILIA DATE: 2000-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 CTACAAGAACTTCTCCTTCAGCAAATTGCTTTTAAAAACCT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.9%; Score 86.2; DB 3; Best Local Similarity 56.0%; Pred. No. 7.6e-12; Matches 191; Conservative 0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 566
LENGTH: 358
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Patent No. 6833446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)..(1110)
US-09-710-861-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: mouse
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US-09-640-211A-566
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684 GAGGAGGCTGGAGAGGATCAAACAGAAGCAGTCTCAGCTCCAGGAGCTCATCCTGCAGCA 743
                                         384 gaagaardecaageecrececarrrrcrccargaagarerereagaagrecagagagaa 443
                                                                                                                                                                                                                               504 caaccacarreraccaaacgaarcagerrargaccagaagaacarcegegegegereren 563
                                                                                                                                                                                                                                                                                564 CGATGCCTTAAATGTGCTAATGGCCATGAACATCATCTCCAAGGAGAAGAAGGAGATCAA 623
                                                                                                                                                                                                                                                                                                                                                                          430 GTGGATGGGCCTTTCAAATTACAGATATGAAAAAATAAAGAAGCTTGAGGAAGTTCGTAA 489
                                                                                                                                                                                                                                                                                                                                                                                                                        624 ATGGATCGGCCTGCCCACCAACTCAGCTCAGGAGTGCCAGAACTTAGAGGTGGAGAGGCA 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      490 AGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATGGAAAAAGGTT 549
202 GATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAA 261
                                                                                                                                   444 Aggaaccaccrocracaargaggregorgacgaggregorgeregoagagricaggegorgcoga 503
                                                                                                                                                                                      316 -----CATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTA
                                                                                            262 AGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTGAAGTC
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ATTORNEY/AGENT INFORMATION:
NAME: CRAMPORD, ARTHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 620-12
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/602,846
FILING DATE: 26-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550 TGATGATCTCCAAAACAT 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            744 AATTGCCTTCAAGAACTT 761
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TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1700 base pairs
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STATE: Virginia
COUNTRY: USA
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US-08-602-846-1
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US-08-602-846-1
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                                                                                                                                                                58 GGCAGAGGACTACGGCATTTCAGCATGAAAGTTTGTAAGAAAGTGGAGAGAAAGGGGCTGG 117
                                                                                                                                                                                                            269 ACAACATACAATGAGGTTGCAGACGAAATTT------ACA-ATTCAGAGCTGAAG 313
                                                                                                                                                                                                                                                        118 ACAACATACAACGAGGTTGCATCTGAATTAGTGGCCGAATTTGTGAATCCAAACAGCACA 177
                                                                                                                                                                                                                                                                                                        314 TCCATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGAT 373
                                                                                                                                                                                                                                                                                                                                                                                                  238 GCACTGAACGTACTGATGGCCATGGACATAATATCAAAGGAGAAAAAGGAGATTAGATGG 297
                                                                                                                  209 GGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAAAAGTTGAAGCCAAAGGAAGA
                                                                        Gaps
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                   Score 85; DB 4; Length 358;
Pred. No. 9.3e-12;
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1. Application US/08428131
| Patent No. 5863757
| GENERAL INFORMATION:
| APPLICANT: La Thangue, Nicholas Barrie
| TITLE OF INVENTION: Transcription Factor DP-1
| NUMBER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS: ADDRESSEE: Nixon & Vanderhye
| STREET: 1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFRENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                        7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 ATGGGCCTTTCAA 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 AAAGGGCTACCTA 310
                   Query Match
Best Local Similarity 62.5<sup>†</sup>
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ubence
LENGTH: 1700 Dance
TYPE: nucleic acid
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LOCATION: 55..1284
US-08-428-131-1
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
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: U.S.A.
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US-08-428-131-1
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Gaps Sequence 1, Application US/08602846
Patent No. 5871901
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAM:
APPLICAM:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE: 12; Length 1700; Indels 3: Nixon & Vanderhye PC 8th Floor, 1100 No. 5871901th Glebe Road Score 83.2; DB 2; Pred. No. 5.1e-11; 0; Mismatches 163; TYPE: nucleic acid and encoded amino acids STRANDEDNESS: double Query Match 7.6%; Best Local Similarity 53.7%; Matches 203; Conservative

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                                                                                                                                                                                202 GATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564 CGATGCCTTAAATGTGCTAATGGCCATGAACATCATCTCCCAAGGAGAAGAAGAGAGATCAA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 gaagaargecaaggecergegecarrirerecargaaggrerergagaaggreeagaggaaggaa 443
                                                                                                                                                                                                                                                                                                               316 -----CATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                          504 CAACCACATICTACCAAACGAATCAGCTTATGACCAGAAGAACATCCGGGGGGGTGTCTA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490 AGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAACAGTT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            684 GAGGAGGCTGGAGAGGATCAAACAGAAGCAGTCTCAGCTCCAGGAGCTCATCCTGCAGCACA 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 GGGAGGGGACTTCGCCAGTTCAGCATGAAGTATGTCAAAAGGTCGAGAGAGCAAGGGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624 ATGGATCGGCCTGCCCACCAACTCAGCTCAGGAGTGCCAGAACTTAGAGGTGGAGAGGCA
                                                                                                                                                                                                                                                                                    262 AGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTGAAGTC----
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                                                                                                                          12;
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                                                                         Score 83.2; DB 3; Length 1 Pred. No. 5.1e-11; 0; Mismatches 163; Indels
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Gene Transcription
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APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matchew
TITLE OF INVENTION: Compositions and Methods:
TITLE OF INVENTION: Modification of Gene Trail
FILE REFERENCE: 11000.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: 2000-08-16
NUMBER OF SEQ ID NOS: 2366
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 465
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Patent No. 6833446
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                                                                         Query Match 7.6%;
Best Local Similarity 53.7%;
Matches 203; Conservative
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Best Local Similarity 57.9
Matches 175; Conservative
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LOCATION:
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US-09-078-596-1
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                        GATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAA 261
                                                                                                                                                                                                                                                                               504 CAACCACATTCTACCAAACGAATCAGCTTATGACCAGAAGAACATCCGGCGCGCGTGTCTA 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             624 ATGGATCGGCCTGCCCACCAACTCAGCTCAGGAGTGCCAGAACTTAGAGGTGGAGAGGCA 683
                                                                      384 GAAGAATGGCZAAGGGCCTGCGGCATTTCTCCATGAAGGTGTGTGTGAAAGGTGCAGAGGAA
                                                                                                                                                                                                                           -----CATGCCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTA
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                                                                                                                                                                          444 AGGAACCACCTCCTACAATGAGGTGGCTGACGAGGTGGTGGCAGAGTTCAGCGCTGCCGA
                                                                                                                          262 AGGAAGAACAAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTGAAGTC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09078596
Patent No. 6150116
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201.4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     550 TGATGATCTCCAAACAT 567
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TYPE: nucleic acid
STRANDEDNESS: double
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470 AAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTC 529
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                                                304 AACATTAGACGAAGAGTTTATGATGCTTTAAATGTACTAATGGCGATGAACATAATTCA 363
                                                                                                                                                                       364 AAGGAAAAAAAAAAATCAAGTGGATTGGCCTGCCTACCAATTCTGCTCAGGAATGCCAG 423
                                                                                                                                                                                                                                                                                     424 AACCTGGAAATCGAGAAGCAGAGGGGGATAGAACGGATAAAGCAGAAGCGAGCCAGCTA 483
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                                                                                                             239 GTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TEAMSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF PILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: 08/09/189,627A
CURRENT PILING DATE: 1998-11-10
PRIOR FILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-09-15
PRIOR RELING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1154
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                                                                                                                                                                                                                                                                                                                                                  530 CAGGAAATCGAAAACAGTTTGATGATCTCCAAACAT 567
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                                                                                                                                                                                                                                                                                                                                                                                                         484 cáagacricccricagcaarrigcrirraaaaaccr
350 AATATTAGGCGGAGAGTGTATGATGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09189627A Patent No. 6159691
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de la Luna, Susana
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Matches 186; Conservative
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; NAME/KEY: CDS
; LOCATION: (1)..(1107)
US-09-189-627A-3
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APPLICANT: La Than
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US-09-189-627A-3
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                                                                                                                   493
                                                                                                                                                                       297 AAGGGGTTACCTAGCACAAGTCCTAATGACCTTGAAGACTTGAAGGCAAAGCGCATGGGA 356
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                                                      237 GCATTGAATGTACTGATGGCAATGGACATCATATCAAAGGACAAGAAGGAAATTCAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: detaluna, Susana
TITLE OF INVENTION: THERSOR TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 81.2; DB 2; Length 1 Pred. No. 1.4e-10; 0; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
FRIOR APPLICATION NUMBER: US/08/723,415B
FILING DATE: 10-SEP-1996
ATFORNEY AGENT INPORMATION:
REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 25,327
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5859199
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7.5%;
Best Local Similarity 55.0%;
Matches 186; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1154 base pairs
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                 CT 495
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MOLECULE TYPE:
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COCATION:
US-08-723-415B-3
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US-08-723-415B-3
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## Sequence 3, Application US/09710861
## Patent No. 6387649
## Patent No. 638769
## Patent
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Pred. No. 1.4e-10;
0; Mismatches 143; Indels 9
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Patent No. 5859199
GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: deLaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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STREET: 1100 No. 5859199th Glebe Rd.
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Matches 186; Conservative
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LOCATION: (1)..(1107)
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LENGTH: 1154
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US-08-723-415B-7
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350 AATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCA 409
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Patent No. 6159691
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
APPLICANT: da la Luna, Susana
TILLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILLING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
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                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION NUMBER: US/08/723,415B
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 15-MAY-1996
ATTONNEY/AGENT INPOMMATION:
NAME: CZAWGOG, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 25,327
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107-916-4100
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                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 55.0%;
Matches 186; Conservative (
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EDNESS: single
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS:
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US-08-723-415B-7
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239 GITTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATT 298
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                                                                                                                                                                                                                                                           Query Match 7.5%; Score 81.2; DB 3; Length 1202; Best Local Similarity 55.0%; Pred. No. 1.4e-10; Matches 186; Conservative 0; Mismatches 143; Indels 9
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Search completed: February 6, 2005, 13:09:14 Job time : 230 secs

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Sequence 33888, A Sequence 4115, Ap Sequence 17642, A Sequence 13906, A Sequence 87351, A Sequence 2033, Ap Sequence 4049, Ap Sequence 43105, A Sequence 30551, A Sequence 35537, A Sequence 35537, A
                                                                                                                                                                                February 6, 2005, 13:09:21; Search time 690 Seconds (without alignments) 9084.062 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/DSO8_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-767-701-17642
US-10-739-930-1190
US-10-425-115-87351
US-10-425-115-2033
US-10-425-114-2003
US-10-425-114-20051
US-10-425-114-20051
US-10-425-114-2051
US-10-425-114-2051
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Sequence 2083, A Sequence 26827, A Sequence 64593, A Sequence 64593, A Sequence 64593, A Sequence 1993, A Sequence 1157, Ap Sequence 1157, Ap Sequence 139, Appl Sequence 139, Appl Sequence 569, Appl Sequence 1394, A Sequence 13117, A Sequence 11218, A Sequence 17885, Sequence 17885, Sequence 56942, A Sequence 6, Appl Sequence 17886, Sequence 56942, A Sequence 6, Appl Sequence 6, Appl Sequence 178785, Sequence 6, Appl Sequence 55942, A Sequence 6, Appl Sequence 
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Sequence 648, App
Sequence 648, App
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Sequence
# US-10-767-795-6106
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# US-10-357-930-20983
# US-10-437-963-63675
# US-10-437-963-64593
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# US-10-160-554-4
# US-10-160-554-4
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## ALIGNMENTS

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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41.6%; Score 452.6; DB 18; Length 1406;
Best Local Similarity 74.7%; Pred. No. 3.1e-98;
Matches 639; Conservative 0; Mismatches 199; Indels 17;
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US-10-437-963-33888
                    Sequence 33888, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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ORGANISM: Oryza sativa
US-10-437-963-33888/c
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Gaps

16; 774;

DB 18; Length Indels

Score 385.4; DB 18; Pred. No. 3.2e-82; 0; Mismatches 176;

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; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_103754C.1
US-10-425-115-4115
                                                                                                    Query Match 35.4%;
Best Local Similarity 74.0%;
Matches 547; Conservative
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; Publication No. US20040214272A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROSa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT PAPLICATION NUMBER: US/10/425,115
; CURRENT PILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
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                                18 GCTGCGGCGGCAGCCGAGCTCACCAGCCTGCGCATCAGCGAAGGAGGAGGGGATCCCTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492 CTTCTCCAGGAAATTGAAAGACCAGCGTGATGACCTCCAGAATATCAAGTTTCGCAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          703 CGAGTTCAATGGTGCACCATTCACATTGCATGATGATCTCTCAATCCTTGAGGGGGGTAAG
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                                                                                                                                                                              GATAAAGATAGGAAGAAGGAGAAAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGC
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Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Cavalic, David K.

APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                763 GCGTAACAGCATAGGAAGA 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTAATAGCGTGAAAAA
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US-10-767-701-17642
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and Other Molecules Associated

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBNE: 38-21(3323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             967 GTGGCGGTGTTGCTTTTTTTTTTTTTTTCTTGTCCACTCGTCCTCACGCAACAGTAGAAG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1027 regagararcagaagarargcagcregrerirrearricaacagcacrecarrigage 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          612 ATGGC---ATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTGGAAA 668
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                                                                                                                                                                                                                                                                                                                       847 cactraggaacagaatrgagaagaaacrgcararrcccaagaacrggaagaacaararg 906
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        547 CTGGAAGAGGACTACGTCAATTTAGTATGAAAGTTTGTGAAAAGGTGGAAAGCAAAGGAA 606
                                                                                                                                                                                                                                                                                                                                                                          432 GGATGGGCCTTTCAAATTACAGATATGAAAAATAAAGAAGCTTGAGGAAGTTCGTAAAG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AGAGGTCTCCGCCAATTTAGTATGAAAGTGTGAAAAGTAGAAAGCAAGAAGAAGAACC 364
                                                                                                               607 GGACAACTTACAATGAGGTTGCAGACGAGCTTGTTGCTGAATTTGCACTTCCAAATAACG
                                                                                                                                                                                                                   667 ATGGAACATCCCCTGATCAGCAACAGTATGATGAGAAAACATAAGACGAAGAGTATATG
                                                                                                                                                                                                                                                                                                                                                                                                                           552 ATGATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAGAATGTTA
                                                                                                                                                                  312 AGTCCATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 492 AACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAACAGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 TGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCCAAAGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                              267 GAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_139556C.1
US-10-424-599-43806
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Pred. No. 1.5e-23;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1087 rccaccaccarrrrrrrcrcraac 1112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43806, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 55.5%;
Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-43806
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21 (53535) B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-739-930-1190

Sequence 1190, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53377)B

FILE REFERENCE: 200-312-18

CURRENT APPLICATION UNDER: US/10/739,930

CURRENT FILING DATE: 200-312-18

NUMBER OF SEQ ID NOS: 11088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AGGGGGTGTTGACCCGGATAAAGATAGGAAGAAGAAGAAGAAGAAGGCTGCGGCACCGAGGATCA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 caggaaatrgaacgacagtrrgargaccrccagaararcaagrrrcgcaaccagrracra 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGAAAGCAAGGGTGGAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTC 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 Aacrdracaccarrcaccrrscarsacsarsrcracarccrrsaascsarcasscratar 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 CAGAGGCCAGCTGAGAGTGCGAATGGTATCTGCCTTCCCATTCTTATTGGTCAAGGCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 AAGTTGGAGGAAACTCGCAAAGAACTCATGATTAGGGTTAAGAACAAGAAAAAACTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                530 CAGGAAATCGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       590 GAAAGCTCAGCAGAGAATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 AGAAAAGCAAGGGTGGAATTGAGATTTCAGAGAACTCAAAGTTTGCTGGTTTCGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470 AAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGACGCACTCCTC
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                                                                                                                                                                                                                                                                                                                                                                        Length 476;
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Pred. No. 9.9e-26;
0; Mismatches 262; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           61; Indels
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US-10-739-930-1190
                                                                                                                                                                                                                                                                                                                                                                     Query Match
18.7%; Score 203.4; DB 18;
Best Local Similarity 79.7%; Pred. No. 1.3e-38;
Matches 240; Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: LIB3476-039-P1-K1-D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.3%;
Matches 346; Conservative
                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                    US-10-767-701-17642
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629 613 719 673

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Sequence 2013, Application US/10425115

| Sequence 2013, Application US/10425115
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Zhou, Yihua
| APPLICANT: Cano, Yought K.
| APPLICANT: APLICANTON: NUMBER: US/10/425,115
| CURRENT APPLICANTON: NUMBER: US/10/425,115
| CURRENT APLICANTON: NUMBER: QU3-4-28
| NUMBER: OF SEQ ID NOS: 369326
| LINGTH: 1483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 ACAITCICGAAGCIICCAGIGICCCCCCCCTICCCGAAGCGGGGGGGTAAIGCGGICCAAA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 cecerreceacadedecececececeres 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTCACATTCCATGATGATCTCTCAATCCTTGAGGGGGTAAGGCGTAACAGCATAGGAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           674 chirceaecriccaccaccaccaracerccranadacaariccarrerecaacaacaac 733
                                                                                                                             254 AGGCACCAGATCCTGATAACCCTAACGCGCAACAATATGATGAGAAAAATATACGACGAA 313
                                                                                   GAGİTTALGALGCITTGAALGİTİCTGALGGCTALGGACATTALATALGALAAAAAĞĞ 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 CGCCTCCCCCCCCGCGGAGCTGCTGCGGCCGCTACCGCCGCCACTGGACCTGACCGGCGTGC
                                                                                                                                                                                                             483 TTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAA
                                                                                                                                                                                                                                            434 AGCTIGTGGGACTGAAAGGTAGGATTGAAAAGAAAAGTGCTTACCTACAGGAGCTACAAG
                                                                                                                                                                                                                                                                                                 AACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAG
                                                                                                                                                                                                                                                                                                                                      494 accaarareraegrerecaaaacerearreaaceaaareaecaareararearreaaa
                                                                                                                                                                                                                                                                                                                                                                                                                        554 Acacccircicaideacicacrifeccairiraicciadircaeaccrcaidira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 AGATCCAGTGGAAGGGCTTGCCGCGTACTAGTATAAGTGACATTGAAGAAATGAAGACGG
                                                                                                                                                                                                                                                                                                                                                                                  A---GAATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660 GGGTGGAAATTGAGATTTCAGATGACTCGAAGTTTGCCCCATTTCGAGTTCAATGGTGCAC
                                            GAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAAGAAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18; Length 1483;
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12.2%; Score 133.4; DB 18;
Best Local Similarity 51.4%; Pred. No. 1.4e-21;
Matches 385; Conservative 0; Mismatches 331;
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Sequence 87351, Application US/204021427241

GENERAL INFORMATION

APPLICANT: La Rosa, Thomas J.

APPLICANT: Royalic, David K.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Worleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Worleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Worleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Worleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: UNMERR: US/10/425,115

CURRENT FILING DATE: 2033-40-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 87351
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                                                                                                                  425 TIGCCCCTGAICAGCAATATGATGAAAAAAAAACATCCGCCGAAGGGTCTATGATGCT
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12.8%; Score 139.8; DB 18; Length 1585;
Best Local Similarity 55.1%; Pred. No. 4.3e-23;
Matches 338; Conservative 0; Mismatches 242; Indels 33; Gaps
                                                                           ATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATGCT
  272 ACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG-
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US-10-425-115-87351
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ORGANISM: Zea mays
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US-10-425-115-87351
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 20051
LENGTH: 1167
TYPE: DNA
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       COCCTCCCCGCGGGGGGCTGCTGCGGCCGCTACCGCCGCACTGGACCTGACCGGCGTGC 83
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Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Liu, Jingdong
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Sonou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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                                                                                                              AAAATGGCCGTGGATTGCGTCAATTTAGCATGAGAGTATGTGAGAAAGTCGAAAGCAAAG 350
                                                                                                                                                              GAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTGAAGTCCATGGCAC 323
                                                                                                                                                                                                                                                                                                                                                TTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAAG 413
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                                                                   TCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAAGCCAAAG
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OTHER INFORMATION: Clone ID: 700347688_FLI
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Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
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US-10-425-114-4049
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; Sequence 36537, Application US/10425114
; Publication No US2004003488A1
; GENERAL INNOFMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Screen, Steven E
; APPLICANT: Abaska, Jack E
; APPLICANT: Abaska, Jack E
; APPLICANT: Abaska, Jack E
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF LIABRITA APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NOS: 73128
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US-10-425-114-36537
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                                                                                                                                                                                                                 DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_138923C.1
US-10-424-599-43105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 181;
                                               ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3170-045-C12_FLI
US-10-425-114-20051
                                                                                                                                                                                                        Score 124.6; DB 1
Pred. No. 1.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 43105, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                             Query Match
Best Local Similarity 57.4%;
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.9
Matches 243; Conservative
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ORGANISM: Glycine
        ORGANISM: Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 GAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTAT 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  643 TCÁGAÁTCTGGÁGATÁGAGAAGCAGAGGCGGATAGAACGGÁTAÁAGCÁGAÁGCGGGCCA 702
                                                                                                              APPLICANT: Lillie, James
APPLICANT: Mangy Youchan
APPLICANT: Wangy Youchan
APPLICANT: Wangy Youchan
APPLICANT: Wangy Youchan
APPLICANT: Wangy Youchan
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             583 Trchahagahahahahahrcangridgarridgccraccraccahrcracrichggahrg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.1%; Score 99.2; DB 14;
58.2%; Pred. No. 3.2e-13;
iive 0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cocks, Benjamin G.
Sugan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR
                              Sequence 10136, Application US/10198846
Publication No. US20030099974A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1456, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
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LOCATION: 1, 2
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 58.2
Matches 199; Conservative
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      JS-10-198-846-10136
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Sequence (106, Application US/10767795)
Publication No. US20040181830A1
GENERAL INFORMATION:
SAPPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5354)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT TILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQUENCE: CONTRACT OF SEQ ID NOS: 117596
                                                       241 CAACGAAATGAGCAATCATATGGTTCAGGAAACACGCCTTCTGGTGGAGTGGCTTTGCCA 300
                                                                                                                                                                                                                                689 AAGTITGCCCATTICGAGTICAAIGGIGCACCATTCACATIGCAIGAICTICTCTAAIC 748
                                                                                                                                                                                                                                                                                       361 cadciadiriridacircaaradcacccarricaagcicardacaacraacarcaracard
                                                                                                                 TICGIATIGGICAAGACAICTAGGAAAGCAAGGGIGGAAAITGAGAITICAGAIGACICG 688
                                                                                                                                                                      TTTATCCTAGTTCAGACCCGACCTCATGCTACTGTGGAAGTTGAAATATCAGAAGTTATG 360
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TTACGTAACCAAACACTGGAAAGCTCAGCAGA---GAATGTTAATGGCATCCGCCTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                            CTAAAAGAAATGCGATTCTGTGGAAGAGAACAACATGACAGCAC 464
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Pred. No. 2.1e-14;
0; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C6102_1
US-10-767-795-6106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 54.9%;
Matches 225; Conservative
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ORGANISM: Gossypium hirsutum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 GCAAAAGAAAAAAAGGAGATACGGTGGATGGGCCTTTCAAATTACAGATATGAAAAAAA 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 ATAGTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAA
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PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
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PRIOR APPLICATION NUMBER: US/60/234,052
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PRIOR PELING DATE: 2000-09-25
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Best Local Similarity 57.8%;
Matches 197; Conservative
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COGANISM: Homo sapiens
US-09-954-456-1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 ATTTATTCAGAGCTG------AAGTCCATGGCACATATTGGTCAAGGGTTTGAT 343
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Pred. No. 3.6e-13;
0; Mismatches 132; Indels 12;
                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/641,643

FILING DATE: 14-Aug-2003

CLASSIFICATION DATA:

APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCTCCAGGAAATCGAAAACAGTTTGATGATCTCCCAAAACAT 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Zeller, Karen J.
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: 9604478
SEQUENCE DESCRIPTION: SEQ ID NO: 1456:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2320 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1456:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 58.1%;
Matches 200; Conservative
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US-09-954-456-1176
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GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
TITLE OF INVENTION: Sets
FILE FOR INVENTION: Sols
CURRENT APPLICATION NUMBER: US/09/954,456

Sequence 1176, Application US/09954456 Patent No. US20020115057A1

Length 1266;

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GenCore version 5.1.6
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20:05:19 ; Search time 165 Second	( tripping of the post of
4, 2005, 20	
February	
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4, 2005, 20:05:19 ; Search time 165 Seconds	(without alignments)	611.785 Million cell updates/sec
February		

1 MAPPRGGAAAAATAALDLTG......SILEGVRRNSIGRAGRATLH 261 US-10-088-830-2 score: Sequence: Perfect

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

2105692 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2001s:\*
geneseqp2003s:\*
geneseqp2003bs:\* A\_Geneseq\_16Dec04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aab67762 Amino aci	Adq36843 Os018989-	Aag22851 Arabidops	Aag22850 Arabidops		Ado62143 Transcrip	Ado63083 Transcrip	Adq36845 Cell prol	4	Adq36855 Cell prol		Aag22852 Arabidops	Aau72529 Arabidops	Abp96848 Arabidops	Adh59560 Dimerisat	Ado63085 Transcrip	Ado62145 Transcrip	Aau72497 Arabidops	Aay32164 Corn DP-2	Aau72572 Arabidops	Aau72559 Arabidops	Adn05730 Antipsori	Abg28057 Novel hum	Aay18026 Murine DP	Aar89212 Transcrip
ID	AAB67762	ADQ36843	AAG22851	AAG22850	AAU72542	AD062143	ADO63083	ADQ36845	AAU72514	ADQ36855	AAB07975	AAG22852	AAU72529	ABP96848	ADH59560	AD063085	AD062145	AAU72497	AAY32164	AAU72572	AAU72559	ADN05730	ABG28057	AAY18026	AAR89212
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% Query Match	9.66	67.5	37.3	37.3	37.3	37.3	37.3	35.7	35.4	35.4	35.0	33.1	32.5	32.5	•	32.5	32.5	32.5	31.6	31.2	•	30.3	30.1	29.5	28.7
Score	1314	890.5	492	492	492	492	492	471.5	466.5	466.5	461	437	428.5	428.5	428.5	428.5	428.5	428.5	416.5	412	406.5	399.5	396.5	389	378.5
Result No.	1	6	m	4	S	φ	7	89	6	10	11	12	13	14	15	16	. 17	18	19	20	21	22	23	24	25

Abb60852 Drosophil	Aag74072 Human col	Adm78625 Human tra	Ado19869 Human PRO	Aar54663 Transcrip	Aaw83389 Caenorhab	Adp12553 Protein e	Abr82450 Human ARP	Adq74871 Human and	Aab67766 Fragment	Aay32161 Impatiens	Aau72563 Arabidops	Aab67767 Fragment	Aab67765 Fragment	Aab33108 Pinus rad	Aau72569 Arabidops	Aau72557 Arabidops	Aab67768 Fragment	Aab33007 Pinus rad	Abg05510 Novel hum
ABB60852	AAG74072	ADM78625	ADO19869	AAR54663	AAW83389	ADP12553	ABR82450	ADQ74871	AAB67766	AAY32161	AAU72563	AAB67767	AAB67765	AAB33108	AAU72569	AAU72557	AAB67768	AAB33007	ABG05510
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445	355	410	410	410	575	345	405	405	26	138	193	26	21	119	142	142	20	120	149
28.5	28.4	28.4	28.4	28.2	26.8	22.9	22.7	22.7	21.7	21.6	21.6	20.6	20.0	19.8	19.8	19.8	19.4	19.3	18.6
375.5	374.5	374.5	374.5	372.5	354	302	299.5	299.5	286	284.5	284.5	272	264	261.5	261	261	256	254.5	245
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation. Amino acid sequence of a wheat E2F-dimerisation partner (DP) protein. AAB67762 standard; protein; 261 AA. (first entry) Triticum monococcum. WO200121644-A2. 11-JUN-2001 29-MAR-2001, AAB67762; RESULT 1 AAB67762 

25-SEP-2000; 2000WO-EP009325.

99ES-00002127. 99ES-00002474. 24-SEP-1999; 11-NOV-1999;

(CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF,

Ramirez-Parra E; Gutierrez-Armenta C,

WPI; 2001-257972/26. N-PSDB; AAF80144. New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.

Claim 7; Fig 1; 77pp; English.

The present sequence represents a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to 3 phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoms protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoms protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue

us-10-088-830-2.rag

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DB 8;
                                                          1 MAPPRGGAAAATAALDLTGVHILEASSVPPLPE----
                  67.5%; Score 890.5; DB 8 63.1%; Pred. No. 4.7e-75;
                                       31; Mismatches
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99US-0123180P.
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99US-0132484P
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                                        Matches 185; Conservative
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                              Similarity
Sequence 294 AA;
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16-APR-1999;
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                                                                                                                                                                   RITGWGLREYSKIVCEKVEAKGRITYNEVADEIYSELKSMAHIGGGFDEKNIRRVYDAF 120
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                                                                                   1 MAPPRGGAAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAP
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                                                     Gaps
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                                Length 261;
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                               Score 1314; DB 4;
Pred. No. 5.6e-115;
                                                     0; Mismatches
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                                                                                                                                                                                                                                         LSILEGVRRNSIGRAGRATLH 261
                                                                                                                                                                                                                                                     ADQ36843 standard; protein; 294 AA
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                             99.68;
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                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                          Best Local Similarity 99.6
Matches 260; Conservative
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              Sequence 261 AA;
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                                                                                                                                                                      61 KKSVSLRSGGGGNAAEREEGGA---NRNGKKEKTGAQRITGMGLREFSKIVSKKVEAKGR
                                                                                                144 YRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVNGIRLP
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                                       Gaps
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                                       41;
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Length 294;
                                       Indels
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PR 04-AUG-1999; 99US-014638BP
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                                                                              37.3%; Score 492; DB 3; Length 344; 47.7%; Pred. No. 1.8e-37; ive 40; Mismatches 68; Indels
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                                                                                                                                                                                                                                                  AAG22850 standard; protein; 385 AA
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99US-0123180P.
99US-012548P.
99US-0125788P.
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                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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05-MAR-1999;
03-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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16-APR-1999;
116-APR-1999;
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28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
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Cell cycle protein; CCP; cell cycle regulation; herbicide;
plant growth regulator; plant development; abiotic stress; biotic stress;
nutrient deprivation; pathogen attack; crop yield; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                    37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cell cycle protein and nucleic acid molecule encoding it useful fregulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.
                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                         Length 385;
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                                                                                                                                                                                                                                                                                                         37.3%; Score 492; DB 3;
larity 47.7%; Pred. No. 2.2e-37;
Conservative 40; Mismatches 68;
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                 9905-0160815P-
9905-0160880P-
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9905-0161404P-
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9905-016193P-
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N-PSDB; AAS96332.
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99US-0160768P.
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27-AUG-1999;
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16-SEP-1999;
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The invention relates to a novel cell cycle protein (CCP) and the polympication and the activity of the polympicate and which binds to the witch modulates the activity of the polympicate and which binds to the polympicate and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP antibody is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, converse to maize, tomato, alfalfa, oilseed rape, soybean, sufflower and canola. CCC maize, tomato, alfalfa, oilseed rape, soybean, sufflower and canola. CCC maize, tomato, alfalfa, oilseed rape, soybean, sufflower and canola. CCC maize, tomato, alfalfa, oilseed rape, soybean, sufflower and canola. CCC concletes characterised by insufficient or excessive production of CCP protein forms which have decreased or absorbers characterised by insufficient or excessive production of CCP protein forms which have decreased or aborted activity. Compounds that bind too modulating about morphology, bichemistry and/or physiology, the length of the CCP polympicies or plant growth regulators. The polymcleotide is useful for modifying cell fate, plant development, of coll division, DNA replication, promotion, stimulation or enhancement of cell division, DNA replication, seed set, seed development, tuber, fruit, lenf formation, seed set, senticody are useful in agriculture to modulate the conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as cold mutrient deprivation, heat, drought, salt stress, or biotic stress such as cold mutrient deprivation, heat, drought, salt stress, or biotic stress such as cold mutrient deprivation, heat, drought, salt stress, or biotic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant quality traits, plant reproduction and seed carear antibodies. CCP protein is useful to screen for and tremand condulate e.g. enhance is useful as an immunogen to courring CCP substrates. The poly 

Sequence 385 AA;

152 LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS 210 97 LKSMAHIG----- OGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKK 151 96 37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNBVADEIYSE . 9 37.3%; Score 492; DB 5; Length 385; 47.7%; Pred. No. 2.2e-37; ive 40; Mismatches 68; Indels 211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248 254 PHATVEVEISEDMQLVHFDFNSTPFELHDDNFVLKTMK 291 Matches 104; Conservative Best Local Similarity Query Match 셤 à 셤 ò ò

Transcription factor G2981, SEQ ID 610. ADO62143 standard; protein; 385 AA. (first entry) 15-JUL-2004. ADO62143; RESULT 6 AD062143 

Plant; transcription factor; transgenic plant; abiotic stress tolerance; semotic stress tolerance; cold tobrance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.

133

Gaps

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The present invention relates to novel plant transcription factor

proteins (1) and nucleotide sequences (II) (ADO61534-ADO63778). The

proteins (1) and nucleotide sequences (II) (ADO61534-ADO63778). The

sequences can be used to produce transgenic plants, which overexpress

(II), where the transgenic plant has an allered trait as compared to a

non-transgenic plant or wild-type plant. The transgenic plant comprises

an altered trait selected from increased tolerance to calid, increased tolerance to cold, increased tolerance to cold,

increased germination in cold, increased tolerance to heat, increased

c germination in heat, increased tolerance to heat, increased

c increased dermination in cold, increased tolerance to disease, including

thompsphate conditions, increased tolerance to disease, including

c increased tolerance to multiple fungal pathogens, increased tolerance

c low phosphate conditions, increased tolerance to

c low phosphate conditions, increased tolerance to

c low phosphate conditions, increased tolerance to

c low phosphate conditions, increased tolerance to

c low phosphate conditions, increased tolerance to

c low phosphate conditions, increased tolerance to

c low phosphate conditions, increased tolerance

c low phosphate conditions, increased tolerance

c lowering, altered dabout meristem development, altered branning pattern,

altered stem morphology, altered wascular tissue structure, reduced

apical dominance, altered trichome density, altered trichome structure, altered seed

c altered stem morphology, altered vascular tissue structure, altered seed

c altered call proliferation, altered col development, altered seed

c altered call proliferation, altered coll expansion, altered seed

c altered sensescence, abnormal embry development, altered brand mass, light

c green or gray leaves, glossy leaves, altered seed ripening, altered seed

c death, lethality when overexpressed, altered seed sigh pattern, altered seed coloration, altered seed coloration, altered seed coloration, altere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seedprenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at five wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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Sherman BK;
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47.7%; Pred. No. 2.2e-37;
tive 40; Mismatches 68
                                                                                                                                                                                                                                                                                                                                          Jiang C, Heard JE, Ratcliffe O, Creelman RA, Riechmann JL, Haake V, Dubell AN, Keddie JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; SEQ ID NO 610; 510pp; English
                                                                                                                                                                                                                                                                                              (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                    17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                                                                                            18-SEP-2003; 2003WO-US030292.
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Matches 104; Conservative
Arabidopsis thaliana.
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23-DEC-2003; 2003WO-US041200.
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                                                                                                                                                                                                                                                                        Sequence 385 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungal disease and particularly Brysiphe, Fusarium and Botrytis, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ACA, reduced sensitivity to ABA, increased sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern,
                                                                 210
           97 LKSMAHIG-----QGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKK 151
                          Plant; transcription factor; transgenic plant; abiotic stress tolerance; semcite stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phobbate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to heat, increased germination in heat, increased tolerance to heat, increased germination in heat, increased tolerance to increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                               LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reuber TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adam LJ, Re
Sherman BK;
                                                                                                                    211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                   254 PHATVEVEISEDMOLVHFDFNSTPFELHDDNFVLKTMK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cliffe O, Creelman RA,
Dubell AN, Keddie JS,
                                                                                                                                                                                                                                                                                                Transcription factor G2981, SEQ ID 1550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1550; 510pp; English
                                                                                                                                                                                                                 ADO63083 standard; protein; 385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratcliffe O,
V, Dubell Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2002; 2002US-0411837P.
17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-2003; 2003WO-US030292
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haake
                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heard JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-330163/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADO63082
                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004031349-A2.
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                                                                                                                                                                                                                                                                     15-JUL-2004
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                                                               152
                                                                                                                                                                                                                                            ADO63083;
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                                                                                                                                                                                     RESULT 7
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altered stem morphology, altered vascular tissue structure, reduced
apical dominance, altered trichome density, altered trichome development,
altered trichome structure, altered coor development, altered shade
avoidance, altered seed development, altered seed ripening, altered seed
avoidance, altered seed development, altered cell differentiation,
altered cell proliferation, altered cell expansion, altered phase change,
altered senescence, abnormal embryo development, altered phase change,
altered senescence, abnormal embryo development, altered programmed cell
cath, lethality when overexpressed, altered necrosis patterns, increased
plant size, increased biomass, large seedlings, dwarfed plants, dark
cypteen leaves, change in leaf shape, increased leaf size and mass, light
green or gray leaves, glossy leaves, altered abaxial/daxial polarity,
altered seed coloration, altered seed size, altered seed shape, large
content, altered seed protein content, altered seed shape, and
content, altered seed protein content, altered seedprenyl content,
altered leaf prenyl lipid content, increased anthocyanin levels, and
decreased anthocyanin levels. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
caterionic format directly from WIPO at
ftp. wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule encoding a cell proliferation-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.3%; Score 492; DB 8; Length 385; 47.7%; Pred. No. 2.2e-37; ive 40; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 PHATVEVEISEDMOLVHFDFNSTPFELHDDNFVLKTMK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell proliferation-related polypeptide #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ36845 standard; protein; 346 AA
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The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related polypeptide. The present sequence is published separately from the main body of the specification as EPO data.
                                                                                                                                                                                                                                                                                                                                                                                                               RKKEKAAAPRIT----GWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAHIGQG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 PDPDNPNTPQFDEKNIRRRVYDALNVLMAMDIISKDKKEIQWKGLPR---TSMSDVEELK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell cycle protein, CCP, cell cycle regulation, herbicide, plant growth regulator; plant development, abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; immunogen.
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KKKKRGPGTRATGPDKGGRGLRQFSMKVCEKVESKGRTTYNEVADELVAEPADPNNNFAS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----FDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELV---NKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTSRK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 APPRGGAAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVD-------PDKD
                                                                                                                                                                                                                                                                                                                                                                             APGMOGGGSAATPA-----ASASASTPASETTVARRLDGLDIOGDDAPSSOPATS
polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops.
                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                 DB 8; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATVEVEISEDMQLVHFDFNSTPFELHDDSFVLK----ALGFSGK 293
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13
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                                                                                                                                                                                                                                                                                                                 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Magyar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acosta JAT,
                                                                                                                                                                                                                                                                               35.7%; Score 471.5; DB 8 39.6%; Pred. No. 1.6e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis partial cell cycle protein CCP33.
                                                                                                                                                                                                                                                                                                               44; Mismatches
                                                                Claim 28; SEQ ID NO 4; 408pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU72514 standard; protein; 376 AA
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                                                                                                                                                                                                                                                                                                               Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boudolf V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-062249/08.
N-PSDB; AAS96304.
                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                Sequence 346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200185946-A2
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                                                                                                                                                                                                                                                                                 Query Match
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The invention relates to a novel cell cycle protein (CCP) and the polymeolectides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for identifying a compound of CCP in a sample. A CCP modulator is useful for modulating the presence of CCP in a sample. A CCP modulator is useful for modulating the presence of CCP in a sample. A CCP modulator is useful for modulating the presence of CCP in a plant such as Arabidopsis thaliana, rice, wheat, mainted and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein or production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polypeptide are useful as herbicides or plant growth regulators. The polypeptide are useful as herbicides or plant growth regulators. The polypeptide is useful for modifying cell fate, plant development, compounds that plant in intiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, S and/or M phase of the cell cycle of a plant, initiation and/or development, under function, dwarfism in plants, creased are as seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, tuber, fruit, leaf formation, shoot and root initiation and/or development, module function, dwarfism in plants, crease such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress and attenuate plant architecture, plant quality traits, plant reproduction and seed development, modulate e.g. enhance crop yields, and attenuate plants or its parts. CCP is useful for avpressing CCP cocurring CCP substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133
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New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 GNAVORKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Gaps
                                                                                                                                                        invention relates to a novel cell cycle protein (CCP) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 PHATVEVEISEDMOLVHFDFNSTPFELHDDNFVLKTMK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.4%; Score 466.5; DB 5
46.3%; Pred. No. 5.2e-35;
iive 38; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell proliferation-related polypeptide #5.
                                                                                                          Claim 34; Page 227-228; 316pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 46.3% Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 376 AA;
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AAG22852
ID AAG22852 standard; protein; 277
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                                                                                                                                                                                                                                              N-PSDB; AAA59702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 299 AA;
                                                                  Misc-difference
                                                                                                   WO200047614-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             transformation)
                                                                                                                                                                  12-FEB-1999;
                                                                                                                                                                                                                                                                                                       the plant.
                                                                                                                         17-AUG-2000
                                                                                                                                                                                                              Lowe KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                   Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
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    %XCCCCCCCCCXXXX141414X222X2X24X22X2X2X2X3X3X3
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                                                                                                                                                                                                                                                                                    The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related polypeptide. The present sequence is published separately from the main body of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 KGLPR---TSINDIEDL@TELVGLKSRIEKKNTYL@EL@DGFVGMOKLIORNEGLYGSG- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VADEIYSELKSMAHI-------GQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 MGLSNYRYEKIKKLEEVRKELV---NKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
 proliferation related polypeptide; cell proliferation; senescence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 PPSGGAQSASTSG-----GSAGSPSSRSEQHVPAAAGMAAGAAASTPISENTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----DKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DP polypeptide; transcription factor; gene transcription; cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                          New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NV--NGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPRGGAAAAATAALDLTGVHILEASSVPP-----LPEAGGNAVQRKGAVDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                              35.4%; Score 466.5; DB 8; Length 379; 37.8%; Pred. No. 5.3e-35; Live 43; Mismatches 77; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    corn transcription factor designated DP.
                                                                                                                                                                                                                                                                 Claim 28; SEQ ID NO 14; 408pp; English.
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           differentiation; stress response
                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                            producing enhanced food crops
                                                                                                                     26-DEC-2002; 2002US-0436565P.
                                                                                                  2003WO-US041200
                                                                                                                                                                                                                                                                                                                                                                     specification as EPO data
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es 111; Conserv
                                                     WO2004061122-A2
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 379 AA;
                                Oryza sativa
                                                                                               23-DEC-2003;
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                                                                          22-JUL-2004
                                                                                                                                                                Cooper B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
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DNA replication; DRTF; differentiation-regulated transcription factor 1; transgenic plant; transformation efficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic plants comprising an expression cassette consisting of a DP nucleic acid, when expressed, the nucleic acid increases the efficiency of plant cell transformation by increasing the number of dividing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 QNLIQRNEQSYGSGNTPSGGVALPFILVQTRPHATVEVEISEDMQLVHFDFNSTPFELHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDLTGVHILEASSVPPLPEAGGNAVQRKG--AVDPDKDRKKEKAAAPRITGWGLREYSKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 IALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELV---NKIRNKKALLQEIEKQFDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNIKLRN-QTLESSAENVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a corn DP (not defined) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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                                                                                                                                                                                                                              /note= "any amino acid encoded by NNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LDING-----DDAPSSQAPTSKKKRRGTRAVGPDKGNR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregory CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.0%; Score 461; DB 3; 40.7%; Pred. No. 1.2e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 DSYVLKEMRFCGREQHDSTQESISNGGESS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 VCEKVEAKGRITYNEVADEIYSELKSMAH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gordon-Kamm WJ, Bailey MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 71-72; 76pp; English.
                                                                                                                                                             Location/Qualifiers
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9905-0139463P

9905-0139463P

9905-01398176P

9905-01398178P

9905-01406535P

9905-01406535P

9905-01406535P

9905-0140623P

9905-0140623P

9905-0141287P

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8 - JUN - 1999;

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28-JUL-1999;
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02-AUG-1999;
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       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 25937.
                                                                                                                                                                                                                                                                                                                           9905-0121825P.
9905-0123180P.
9905-0125788P.
9905-0126785P.
9905-0126785P.
9905-0128744P.
9905-0128744P.
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9905-013884P.
9905-0131449P.
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9905-0131448P.
9905-0131448P.
9905-013148P.
9905-0131458P.
                                                                                                                                                                                                                                                                                              2000EP-00301439
                                                      (first entry)
                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                             25 - FEB - 1999, 05 - MAR - 1999, 05 - MAR - 1999, 22 - MAR - 1999, 23 - MAR - 1999, 29 - MAR - 1999, 29 - MAR - 1999, 29 - MAR - 1999, 23 - MAR - 1999, 23 - MAR - 1999, 24 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - MAY - 1999, 25 - M
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                                                      17-OCT-2000
                                                                                                                                                                                                                           EP1033405-A2
                                                                                                                                                                                                                                                             06-SEP-2000
                     AAG22852;
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Cell cycle protein; CCP; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; immunogen.

Arabidopsis thaliana.

WO200185946-A2.

15-NOV-2001.

Arabidopsis cell cycle protein CCP16.

(first entry)

26-FEB-2002

AAU72529;

AAU72529 standard; protein; 292 AA

RESULT 13 AAU72529

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VCEKVEAKGRITYNEVADEIYSELKSMAHIG-----QGFDEKNIRRRVYDAFNVLIALRV 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.1%; Score 437; DB 3; Length 27 Best Local Similarity 50.3%; Pred. No. 2e-32; Matches 91; Conservative 32; Mismatches 52; Indels
                                                                                                                                                                          99US-0157865P.
99US-0158029P.
99US-0158232P.
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13-OCT-1999;
13-OCT-1999;
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14-0CT-1999;
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New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.

Claim 34; Fig 16; 316pp; English.

De Veylder L, Acosta JAT, Magyar Z;

14-MAY-2001; 2001WO-IB001307. 12-MAY-2000; 2000US-0204045P

(CROP-) CROPDESIGN NV.

Inze D, Boudolf V, WPI; 2002-062249/08. N-PSDB; AAS96319.

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The invention relates to a novel cell cycle protein (CCP) and the polymorlectides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to thee polypeptide and an anti-CCP antibody is useful for adulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CC cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, candleid and olypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or percent activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or polymeptide are useful as herbicides or plant growth regulators. The polymucleotide is useful for modifying cell fate, plant development, of polymeptide are useful as herbicides or plant growth regulators. The polymucleotide is useful for modifying cell fate, plant development, the cell cycle of a plant, initiation, promotion, promotion, stimulation or enhancement of cell division, blant polymucleotide stimulation or enhancement of cell division, but replication, seed set. comessence, tolerance or resistance to stress. CCP, the polymucleotide and the anti-CCP antibody are useful in agriculture to modulate the conditions, heat, drought, salt stress, or biotic stress such as cond, mutrient deprivation, heat, drought, salt stress, or biotic stress such as cond, mutrient deprivation, heat, drought, salt stress, or biotic stress such as cond attendance conditions, heat, drought, salt stress, or biotic stress such as immunogen to generate antibodies. CCP protein is useful for expressing CCP protein, to detect CCP munk, or engeneral essentes and to generate antibodies. CCP protein is sequence represented and to development.

CC protein levels or a genetic lesson in a CCP protein of end
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IAKEKKEIRWMGLSNYRYEKIKKLEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQ 188
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Gaps

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IndelB

69

49; Mismatches

Length 292;

32.5%; Score 428.5; DB 6; 41.3%; Pred. No. 1.4e-31;

Query Match
Best Local Similarity 41.3
Matches 88; Conservative

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Sequence 292 AA;

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 100 MAHIGO-----GFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLE

Sequence 292 AA;

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The present invention describes a method for modulating endoreduplication in a plant, or a part of the plant. The method comprises modifying the expression or activity of an E2F and DP gene or polypepitide. Also described: (1) a transgenic plant cell overexpressing an E2F or E2Fa gene, or an E2F and DP gene or an E2Fa and DPs gene, where the E2F or E2Fa gene or the DP or DPs gene is under the control of a tissue or celltype specific promoter; (2) a transgenic plant, or a part of the plant, comprising the cells described above; (3) a progeny of the plant described above; and (4) a plant material obtained from the plant described above; The method is useful in modulating plant cell cycle proteins by modifying the expression or activity of an E2F and DP gene or polypeptide. The present sequence represents Arabidopsis thaliana DP, which is used in the exemplification of the present invention
                                                                                                                                                   Modulating endoreduplication in a plant, or a part of the plant, comprises modifying the expression or activity of an B2Fa and DPa gene or
                                                                                                                              100 MAHIGQ-----GFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLE 153
                                                                                                                                                                                               154 EVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAEN-VNGIRLPFVLVKTSRK 212
                                                                                                                                                                                                                    66
                                                                                               86
                                                                                  40 VQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKS
                                  Gaps
                                7;
Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana; modulation; endoreduplication; plant; transgenic plant; cell cycle; E2F; DP.
             .4e-31;
les 69; Indels
32.5%; Score 428.5; DB 5;
                                                                                                                                                                                                                                                               ARVEIEISDDSKFAHFEFNGAPFTLHDDLSILE 245
                                                                                                                                                                                                                                                                                AVVEIEISEDMOLVHLDFNSTPFSVHDDAYILK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Segers G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana DP protein SEQ ID NO:4.
               ; Pred. No. 1.4e
49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 26-27; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                ABP96848 standard; protein; 292 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-2002; 2002WO-EP009504
                  41.3%;
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                                88; Conservative
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             Best_Local Similarity
Matches 88; Conser
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                                                                                                                                                                                                                                                               213
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The present invention relates to increasing the cell number of specific cell types, specific tissues or specific organs in a plant comprises modulating the expression and/or the activity in the specific cell types, specific tissues or specific organs of the plant E2F transcription factor. The E2F transcription factor or its homologue, derivative or fragment, is useful for prolonging the period of cell division in certain cells and tissues, for increasing the size of cotyledons, for enhancing cell proliferation after seed germination, for enhancing stress resistance of seedlings, for obtaining seedlings with enhanced vigor, for obtaining plants that have increased growth or number of organs, for obtaining plants having more cells in a particular tissue, for obtaining plants having an increased size of organs or having increased yield, for stimulating differentiated cells to re-enter the cell cycle, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying cell number, architecture and yield of plants comprises modulating the expression and/or the activity of members of the plant E2F transcription factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inze D, Mironov V, Broekaert W;
                                                                                                                                                                               E2F transcription factor; Gene therapy; stress resistance; differentiation signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; SEQ ID NO 4; 41pp; English.
                                      Ä
                                      ADH59560 standard; protein; 292
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                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2001; 2001EP-00870198
                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Veylder L,
                                                                                                           (first entry)
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                                                                                                                                               Dimerisation partner.
                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-371815/35.
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                                                                        ADH59560;
RESULT 15
                     ADH59560
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overriding the cell differentiation signals, or for altering cell shape. The present sequence represents the dimerisation partner.
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Sequence 292 AA;

Query Match 32.5%; Score 428.5; DB 7; Length 292; Best Local Similarity 41.3%; Pred. No. 1.4e-31; Matches 88; Conservative 49; Mismatches 69; Indels 7; Gaps

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Search completed: February 4, 2005, 20:30:04 Job time : 168 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 4, 2005, 20:21:34; Search time 39 Seconds (without alignments) 643.912 Million cell updates/sec

Perfect score:

US-10-088-830-2 1319 1 MAPPRGGAAAAATAALDLTG......SILEGVRRNSIGRAGRATLH 261

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Seguence:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIR 79:\* Database

pir1:\*
pir2:\*
pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	transcription fact		hypothetical prote	transcription fact				hypothetical prote	ᄆ	hypothetical prote	യ			m	translation initia	hypothetical prote	hypothetical coile	transcription fact		transcription fact	surface membrane	E2F-1 transcriptio	glucuronosyltransf	hypothetical prote			hypothetical prote	Н	
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de	Query Match	34.6	32.5	30.1	28.7	8	28.5		26.8	9.7	9.1	8.8	8.5	8.5	8.5	8.5	8.5	8.5	8.1	8.1	8.0	7.9	7.8	7.7	7.7	7.7	7.7	7.7	7.7	
	Score	456	428.5	396.5	378.5	378.5	375.5	374.5	354	128.5	120.5	116.5	112.5	112.5	112.5	112	108.5	108.5	107	107	105	104.5	102.5	101.5	101.5	101	101	101	101	
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RESULT 2
148268
D.2 transcription factor-like - Arabidopsis thaliana
N/Alternate names: protein T22P11.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

myosin heavy chain	hypothetical prote	conserved hypothet	chromosome segrega	hypothetical profe	probable ATP /GTP	ATPase involved in	hypothetical prote	bps2 protein - Des	conserved hypothet	embryonic muscle m	protein F10C1.2a [	E2F-5 - mouse	transcription fact	1-phosphatidylinos	hypothetical prote
818199	D84829	A70387	I54383	D71453	A81385	G97236	T05634	S22195	F75103	A59236	D88163	I48338	JC5833	A28821	869023
N	N	N	7	7	~	N	N	~	7	~	~	7	~	7	7
1039	416	978	1233	279	728	1163	1496	582	880	1927	558	335	346	1216	410
7.6	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.3
100	99.5	99.5	66	98.5	98.5	98.5	98.5	86	98	86	97.5	97	97	97	96.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

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C;Accession: T48364
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24492
A;Recession: T48364
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-413 *eBEV-
A;Acsidues: 5
A;Introns: 84/2; 128/1; 142/3; 163/3; 212/3; 249/1; 279/3; 303/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AKGRITYNEVADEIYSELKSMAHIG-----QGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 KLRNQTLESSAENVN-GIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription factor-like protein - Arabidopsis thaliana
N;Alternate names: protein F12E4.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSK------IVCEKVE
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A;Residues: 'M',33-49 <ZHA2>
A;Cross-references: EMBL:U35117; NID:g1008545; PIDN:AAC50642.1; PID:g1008546
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A, Map position: 3423-3423
A, Note: DKE243443222. 1
C, Superfamily: transcription factor DP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                 A; Gene: GDB: TFDP2; DP2
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A; Scatus: preliminary
A; Molecule type: mRNA
A; Residues: 1-416 -ANG>
A; Cross-references: UNIPROT:Q9UG28; EMBL:AL080206
A; Experimental source: adult testis; clone DKF2P434G22
A; Experimental source: adult testis; clone DKF2P434G22
A; Experimental source: adult testis; clone DKF2P434G22
A; Title: In vivo association of E2F and DP family proteins.
A; Accession: A57381
A; Accession: A57381
A; Accession: A57381
A; Accession: A57381
A; Scatus: preliminary
A; Molecule type: mRNA
A; Residues: 'M', 33-416 <WUN>
A; Residues: 'M', 33-416 <WUN>
A; Cross-references: GB:L40386; NID:g703084; PIDN:AAA69016.1; PID:g703085
A; Title: Cloning and characterization of human DP2, a novel dimerization partner of E2F.
A; Accession: 17297; WUID:95303470; PMID:7784053
A; Accession: 177297; MUID:95303470; PMID:7784053
        C;Accession: T48268
K;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24490
A;Recession: T48268
A;Accession: T48268
A;Accession: T48268
A;Accession: T48268
A;Accession: T48268
A;Accession: T48268
A;Croser-references: UNIPROT:Q9LZ55; EMBL:AL162971
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A;Residues: 1-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein DKFZp434G222.1 - human (fragment)
NjAlternate names: E2F dimerization partner 2
C;Species: Homo sapiens (man)
C;Species: Ja-ul-1999 #sequence revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12511; A57381; I37297; I39180
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z1757
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A;Molecule type: mRNA
A;Residues: 'M',33-143,'Q',144-416 <ZHA1>
A;Cross-references: EMBL:U18422; NID:g604478; PIDN:AAB60378.1; PID:g604479
A;Accession: I39180
A;Accession: I39180
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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32.5%; Score 428.5; DB 2; Length
Best Local Similarity 41.3%; Pred. No. 4.3e-21;
Matches 88; Conservative 49; Mismatches 69; Indels
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11-Nov-1994 #sequence revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: B48585; S38372; S38371
C;Accession: B48585; S38372; S38371
Genes Dev. 7, 1850-1861, 1993
A;Title: Heterodimerization of the transcription factors E2F-1 and DP-1 leads to cooperat.
A;Reference number: A48585; MUID:94010284; PMID:8405995
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A;Residues: 1-410 <HELD:
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A;Recession: S18372
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A;Residues: preliminary
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R;Girling, R.; Partridge, J.F.; Bandara, L.R.; Burden, N.; Totty, N.F.; Hsuan, J.J.; La 'Mature 365, 468, 1993
A;Title: A new component of the transcription factor DRTF1/E2F.
A;Reference number: S38371; MUID:94019777; PMID:8413592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 KIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 PLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVA
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     30.1%; Score 396.5; DB 2
33.9%; Pred. No. 8.4e-19;
tive 52; Mismatches 96
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A;Residues: 388-410 <GI2>
A;Crose-references: EMBL:X72310
C;Superfamily: transcription factor DP
C;Keywords: DNA binding; transcription factor
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C;Accession: A48585
R;Helin, K.; Wu, C.L.; Fattaey, A.R.; Lees, J.A.; Dynlacht, B.D.; Ngwu, C.; Harlow, E. Genes Dev. 7, 1850-1861, 1993
A;Title: Heterodimerization of the transcription factors E2F-1 and DP-1 leads to cooperat A;Reference number: A48585; MUID:94010284; PMID:8405995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 KGRTTYNEVADEIYS-ELKSMAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 GLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESS----AE 195
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                  21 VHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEA
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                       A;Cross-references: UNIPROT:Q24318; GB:X79708; NID:g516866; PID:g516867
C;Genetics:
A;Gene: Flybase:Dp
A;Gene: Flybase:Dp
C;Superfamily: transcription factor DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 NVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILB 245
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                                                                                                                                                                                                                              Length 377;
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1 Similarity 39.1%; Pred. No. 1.8e-17;
90; Conservative 49; Mismatches 68;
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42.0%; Pred. No. 2.3e-17;
tive 42; Mismatches 60
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A; Residues: 1-377 < DYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S:
Matches 86,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor DRTF1 chain 1 - mouse
NyAlternate names: transcription factor DP-1
NyAlternate names: transcription factor DP-1
Syspeciaes: Mus musculus (house mouse)
C;Dete: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Dec-1999
C;Accession: S30049; S34572
C;Accession: S30049; S34572
NyAlthing, R.; Partridge, J.F.; Bandara, L.R.; Burden, N.; Totty, N.F.; Hsuan, J.J.; la Nature 362, 83-87, 1993
A;Title: A new component of the transcription factor DRTF1/E2F.
A;Reference number: S30049; MUID:93188967; PMID:8446173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor DP - fruit fly (Drosophila melanogaster)

(species: Drosophila melanogaster

(species: Drosophila melanogaster

(species: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 09-Jul-2004

(spacession: B55745

R.Dynlacht, B.D.; Brook, A.; Dembski, M.; Yenush, L.; Dyson, N.

R.Dynlacht, B.D.; Brook, A.; Dembski, M.; Yenush, L.; Dyson, N.

A;Title: DNA-binding and trans-activation properties of Drosophila B2F and DP proteins.

A;Reference number: A55745; MUID:94294381; PMID:8022787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <GIR2>
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                                                                                                                                                                                                                                                                                                         50 KDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
                                     106 GFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRN 165
                                                                                                                                                                KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEİSD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 KDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNRKGEK-----NGKGLRHFSMKVCEKVQRKGTTSYNEVADELVAEFSAADNHILPNES 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 GFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEISD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
R,Molecule type: protein
C,Superfamily: transcription factor DP
C,Keywords: DNA binding; transcription factor
F,84-204/Domain: DNA binding #status predicted <DNA>
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A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.7%; Score 378.5; DB 2; 42.4%; Pred. No. 1.3e-17; ive 41; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                           DSKFAH-FEFNGAPFTLHDDLSILE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSKFAH-FEFNGAPFTLHDDLSILE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                 | [| : | |: | : |: |: |: |: | D-KFEYLENFDNT-FEIHDDIEVLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: S30049
A,Molecule type: mRNA
A,Residues: 1-429 <GIRI>
A,Cross-references: EMBL:X72310
A,Accession: S34572
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Best Local Similarity
                                                                                                                                                                                                                                                         166
                                                                                                                                                                                                                                                                                                                                                                                           222
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9.1%; Score 120.5; DB 2; Length 470;
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N;Alternate names: Ap12 protein; retinoblastoma-associated protein; retinoblastoma-bindi
C;Specias: Home sapiens (man)
C;Date: 22-Oct-1996 Heaquence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Date: 22-Oct-1996 Heaquence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Date: 22-Oct-1996 Heaquence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Date: 22-Oct-1996 Heaquence revision 01-Nov-1996 #text_change 09-Jul-2004
R;Neuman, E.; Sellers, W.R.; McNeil, J.A.; Lawrence, J.B.; Kaelin Jr., W.G.
A;Title: Structure and partial genomic sequence of the human E2F1 gene.
A;Reference number: JC4929
A;Status preliminary; nucleic acid sequence not shown
A;Molecula Fype: DNA
A;Residuse: 1-437 <ARBJ.
A;Residuse: 1-437 <ARBJ.
A;Residuse: 1-437 <ARBJ.
A;Cross-references: UNIPROT: Q01094; GB:U47675; NID:g1594281; GB:U47676; NID:g1594282; GE
A;Experimental source: placenta
R;Shan, R; Zhu, X; Chen, P.L.; Durfee, T.; Yang, Y.; Sharp, D.; Lee, W.H.
Mol. Cell. Biol. 12, 5620-5611, 1992
A;Title: Molecular cloning of cellular genes encoding retinoblastoma-associated proteins
A;Reference number: A45032
A;Accession: A4503
A;Accession: A4503
A;Reference mumber: A45032; MUD:93078763; PIDN:AAB24289:1; PID:g260574
A;Cross-references: GB:S49592; NID:g260573; PIDN:AAB24289:1; PID:g260574
A;Cross-references: GB:S49592; NID:g260573; PIDN:AAB24289:1; PID:g260574
A;Residuse: V.A.; Vidal, M.; Dyson, N.; Harlow, E.; Fattaey, A.
Cell 70, 337-350, 1992
A;Title: A CNNA encoding a pRB-binding protein with properties of the transcription fact
A;Accession under: A4998; MUD:92346720; PMID:1638634
R;Barlow, K.

Bubmitted to the EMBL Data Library, December 1995

A;Reference number: 21995

A;Accession: T25207

A;Accession: T25207

A;Accession: Freliminary; translated from GB/EMBL/DDBJ

A;Acceule type: DNA

A;Residues: 1-598 «MIL>
A;Residues: 1-598 «WIL>
A;Cross-references: UNIPROT:Q22703; EMBL:Z68319; PIDN:CAA92699.1; GSFDB:GN00020; CESP:TZ
C;Genetics:
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A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rosiduces: 1-312,'S',314-321,'N',323-328,'T',330-437 <HEL>
A;Rosiduces: 1-312,'S',314-321,'N',323-328,'T',330-437 <HEL>
A;Cross-trefexences: GB:M96577; NID:g181917; PIDN:AAA35782.1; PID:g181918
A;Experimental source: Nalm 6 pre-B leukemia cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:110015, NCBIP:110016)
A;Note: sequence extracted from NCBI backbone (NCBIN:110015, NCBIP:110016)
A;Note: Sequence extracted from NCBI backbone (NCBIN:110015, NCBIP:110016)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 LNVLLAMNITKSKKDIRWIGLPASASQEISRLEEEKSRREASISSKKQALEEMVLQIVS 191
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                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 3/3; 115/3; 204/2; 227/2; 260/1; 298/1; 363/1; 424/3; 478/3; 565/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                            26.8%; Score 354; DB 2; Length 598; 41.3%; Pred. No. 7.9e-16; ive 34; Mismatches 67; Indels
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Best Local Similarity 41.3*
Matches 78; Conservative
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IHDDFEILK 259
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                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:T23G7.1
A;Map position: 2
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A,Title: Autoregulatory control of E2F1 expression in response to positive and negative 1
A,Reference number: 154091; MUID:95047311; PMID:7958836
                                                                                                                                                                                                                                                                                                                  A;Accession: I54091
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-88, R', T',122-123, TPR',127, 'QRR',297-299, 'PRR',308-309, 'RA',312,'C' <RES: C;Genetics: CB:S74230; NID:G712816; PIDN:AAD14150.1; PID:G4261850
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C,Species: Caenorhabditis elegans
C,Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C,Accession: T31602
R,Wallis, J.
R,Wallis, J.
R,Wallis, J.
A,Reference number: Z21046
A,Accession: T31602
A,Accession: T31602
A,Accession: T31602
A,Accession: DNA
A,Wolecule type: DNA
A,Wolecule type: DNA
A,Residues: 1-470 <WIL.>
A,Cocss-references: EMBL:AL117203; NID:e1549827; PIDN:CAB55117.1; CESP:Y48C3A.t
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124 EKSRYETSLNLTTKRF---LELLSHSADGVVDLNWAAEVLKVOKRRIYDITNVLEGIQLI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ILFATPQAPRPTPSAPRPALGRPPVKRRLDLETDHQYLAESSGPARGRGRHPGKGVKSPG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 AKE-KKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----RQLÓESÉQÓLDHLMNÍCTTQL 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 APAGGPCAPALBALLGAGALRLDSSQIVIISAAQDASAPPAPT--GPAAPAAGPCDPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 ----KDRKKEKAAAPR------ITGWGLREYSKIVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SVPPLPEAGGNAVORKGAVDPD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GDB:E2F1
A;Gene: GDB:134661; OMIM:189971
A;Gross-references: GDB:134661; OMIM:189971
A;Gross-references: GDB:134661; OMIM:189971
A;Gross-references: 87/3 118/1 191/2 242/2 280/3 356/1
C;Keywords: DNA binding; transcription factor F;G7-108/Region: cyclin box #status predicted F;118-190/Domain: DNA binding #status predicted <Pi191-241/Region: 7-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 VEAKGRITYNEVADEIYSELKSMAHIGOGFDEKN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:Y48C3A.t
A;Introns: 52/3; 156/2; 206/2; 237/3; 332/1; 386/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.7%; Score 128.5; DE
Best Local Similarity 24.3%; Pred. No. 0.32;
Matches 64; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AKKSKNHİQWLG-SHTTVGVGGRLEGLTQDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 APPRGGAAAATAALDLTGVHILEAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 RLLS--EDTDSQRLAYVTCQDLR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 TLESSAENVNGIRLPFVLVKTSR 211
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14;

Gaps

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Cyccession: T27066
CyAccession: T27066
CyAccession: T27066
RyMcMurray, A submitted to the EMBL Data Library, January 1998
RyMcMurray, A submitted to the EMBL Data Library, January 1998
A;Reference number: Z20305
A;Accession: T27066
A;Accession: T27066
A;Accession: T27066
A;Accession: T27066
A;Accession: T27066
A;Accession: T27066
A;Accession: T27066
A;Accession: T27066
A;Accession: T27066
A;Accession: T2706
A;Cross-references: UNIPPOT:045958; EMBL:AL021493; PIDN:CAA16394.1; GSPDB:GN00023; CESP:)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-717 <WIL>
A;Cross-references: UNIPROT:045959; EMBL:AL021493; PIDN:CAA16395.1; GSPDB:GN00023; CESP:)
A;Experimental source: clone Y51A2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 NSPVDEKFESQPKTLMLNVG------KVQDLFNVLVDLSSIENKFKKLKRKVMLLS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 PINLDKHLIRVKVEGILEELQQLTLSYYEKLLPPQPYRKYKKLLKKLINGRKEFADKVDN 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 KKAL---LOEIEKOPDDLONI-----KLRNOTLESSAENVNGIRLPFVL---VKTSRKAR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368-NSPVDEKFESOPKTLMLNVG------KVQDLFNVLVDLSSIENKFKKLKRKVMLLS 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKAL---LOEIEKOFDDLONI-----KLRNOTLESSAENVNGIRLPFVL---VKTSRKAR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y51A2B.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bacession: T27067
R;McMurray, A
R;McMurray, A
R;McMurray, A
R;Reference number: Z20305
A;Reference number: Z20305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 NEVADEIY-SELKS-MAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 -----RYEK-IKKLEEVRKELVNKIRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 NEVADEIY-SELKS-MAHIGOGFDEKNIRRRVYDAFNVLIALRVIAKEKK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Map position: 5
A,Introns: 8/1; 33/1
C,Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33
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A;Introns: 8/1; 33/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 VEIEISD----DSKFAHFEFNGAPFTLHDDL-SILEGVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 ---EISDKMKENSNNKTFVMNALSFNKSDSIKSIVSSVQ 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
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8.5%; Score 112.5; DB 2;
Best Local Similarity 26.0%; Pred. No. 6.6;
Matches 57; Conservative 35; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
8.5%; Score 112.5; D:
Best Local Similarity 26.0%; Pred. No. 6.6;
Matches 57; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Gene: CESP: Y51A2B.6a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Durine NTPase [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #text_change 09-Jul-2004 C;Accession: B90395 C;Accession: B90395 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan John, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Shilohous Solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90395
                                                                                                                                                                 64 IDLGSIP-----GGSEQQQHEDGAAAAGSPKEVFRSQQSLGLITQRFMSLRQRNEVL-- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 KVEAKGRITYNEVADEIYSELKSMAHIGQGFDEKNI-RRRVYDAFNVLIALRVIAK-EKK 134
                                                                                                                                                                                                                                                                                                                                                                                                                            135 EIRWMGLSNYRYE-----KIKKLEEVRKELVNKIRNKKALLQ-----EIEKQFDDLQNI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 KLRNQTLESSAENVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEF-----NGAP---- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| :| | ::: | | ::: | | ::: | | :::| | | :::| | | :::| | | | :::| | | | :::| | | | :::| | | | :::| | | | :::| | | | :::| | | | :::| | | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 EYSKIVCE--KVEAKGRITYNEVA--DEIYSELKSMAHIGOGFDEKNIRRRVYDAFNVLI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 -----VNKIRNKKALLQEIEKQ----FDDLQNIKLRNQTLESSAENVNGIRLP--- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 FVLVKTS-------RKARVEIEISD-----DSKFAHFEFNGAPFTLHDDLS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : :|||
637 YNELKTSLDAYNLSLKEKENRKSRIEGELESLEKDIEEISNRIANYELQ-----LKDREK 691
                                                                                                                 24 LEASSVPPLPEAGGNAVQR-----KGAVDPDKDRKKEKAAAPRITG--WGLREYSKIVCE
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 ALRVIAKEKKEIR-----WMGLSNYRYEKI------KKLEEVRKEL----
                                            79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81;
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8.8%; Score 116.5; DB 2; Length 864;
Best Local Similarity 21.9%; Pred. No. 4.5;
Matches 56; Conservative 48; Mismatches 71; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71; Indels
                                            88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 -FTL------HDDLSILEGVRRNSIGRAGRATL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y51A2B.6a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 LFTNDPPEYGDEEDEDDVKKLSSQKRFETSEALRVTL 301
    s; Pred. No. 1.2;
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: : | |:::|
692 IINAINKLEKIRSALG 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 ILEGVR-----RNSIG 253
23.1%;
    Best Local Similarity 23.1%
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-864 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                 494 D-----NDTAE-------LVATEFGHTVKRVSEADVEEGFIGADDHDEHM 531
                         3 PPRG---GAAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVDPDXDRKKEKAAA
                                                                                                                                    60 PRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYS--ELKSMAHIGQGFDEKNIRRRVY
                                                                                                                                                                                                                                                                                                     444 AVEQARVAREVVIPDVITV------QELSNRMAVRGVDIIKFLMRQGVMLKINDVI
                                                                                                                                                                                                                                                                                                                                                           178 DDLONIKLRNOTLESSAENVNGIRLPFVLVKT----SRKARVEIE---ISDDSKFAHF
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A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Recence number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70356
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1156 AQP>
A;Residues: 1-1156 AQP>
A;Cross-references: UNIPROT:066878; GB:AE000699; NID:92983238; PIDN:AAC06839.1; PID:9298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87254
R;Accession: B87254
B; Laub, M.T.; DeBdy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon J.; Exmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. US.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus
A;Reference number: A87299; MUID:21173698; PMID:11259647
A;Status: preliminary
A;Residues: 1-1037 <STO>
                                                                                                                                                                                                                                        chromosome assembly protein homolog - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: B70356
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
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C;Genetics:
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22.5%; Pred. No. 11;
:ive 41; Mismatches 106; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 NYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQN-----
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                                                      215 VEIEISD----DSKFAHFEFNGAPFTLHDDL-SILEGVR 248
                                                                                                       ---EISDKMKENSNNKTFVMNALSFNKSDSIKSIVSSVQ 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
8.5%; Score 112.5; DB 2;
Best Local Similarity 22.4%; Pred. No. 12;
Matches 50; Conservative 44; Mismatches 76;
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C;Superfamily: chromosome segregation protein SMC1
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Best Local Similarity 22.5
Matches 63, Conservative
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Q67754 homo sapien
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1 MAPPRGGAAAAATAALDLTG.....SILEGVRRNSIGRAGRATLH
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Q7XZ14
Q84VD5
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Q9CR754
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TDP DROME
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Q8CPEO
Q9V6MO
TDP1 HUWAN
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:000567; C:transcription factor activity; IEA.
GO; GO:000074; P:regulation of cell cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00316; E2F_TDP.
InterPro; IPR00316; E2F_TDP.
Figh: PF02319; E2F_TDP.
Figh: PF02319; E2F_TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 261 AA; 29262 MW; 5008D8F193163A28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONIKLRNOTLESSAENVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAHIGQGFDEKNIRRRVYDAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE_20562804; PubMed=11108846; DOI=10.1016/S0014-5793(00)02239-0; Ramirez-Parra B., Gutierrez C.; "Characterization of Wheat DP, a heterodimerization partner of the plant E2F transcription factor which stimulates E2FZDNA binding."; PEBS Lett. 486:73-78(2000).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SUBCELLULAR LOCATION: Locar (By similarity).
-!- SIMILARITY: Belongs to the E2F/DP family.
-!- SIMILARITY: BLOGATION: Locar (By Similarity).
-!- SIMILARITY: BLOGATION: Locar (By Similarity).
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Triticum sp.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                           261 AA
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           TDP1 CAEEL
Q9GTZ7
                                                            Q6PBR6
TDP2 MOUSE
Q9NZ54
                                                                                                            Q7KWP1
Q8SKS9
E2F1 HUMAN
Q9BIE8
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RA50 SULSO
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28C8M7
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Matches 258; Conservative
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Name=B1144604.21;
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
         Last sequence update)
Last annotation update)
 Created)
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Putative DP protein.
                                                                                                                                                                                                                                                                                                                                               Q8S182; -
                                                                                          NCBI_TaxID=39947;
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                                                                                                                                                                                                       Gaps
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                                                                                                                                                Oryža sativa (japonica cultivar-group).
Sukaryota, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.5%; Score 890.5; DB 2; Length 294; 63.1%; Pred. No. 6.5e-50; ive 31; Mismatches 36; Indels 41
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                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DP protein.
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                                                                                    294 AA
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             LSILEGVRRNSIGRAGRATLH 261
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                                                                                    PRELIMINARY;
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SABARI T., Matsuncto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Sabaki T., Matsuncto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Asabaki T., Matsuncto T., Yamamoto K., Antonio B.A., Kanamoti H., Antaka K., Hayashi M., Hardad M., Hardad M., Hardad M., Hardad M., Hardad M., Hardad M., Hardad M., Hardad M., Hardad M., Hishita S., Honda M., Ichikawa Y., Idonuma A., Iijina M., Ikeda M., Rasaswa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Andrias M., Makabanima M., Nakamichi Y., Nakai Y., Nakamita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Nakamiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M., Shomura M., Songui S., Yoshihara R., Yamane H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Imama H., Endo T., Ito H., Hahn J.H., Kim H.I., Bun M.Y., A Zhong H., Imama H., Endo T., Ito H., Hahn J.H., Kim H.I., Bun M.Y., M. The genome sequence and structure of rice chromosome I.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 NYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLONIKLRNOTLESSAENVNGIRL 202
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60; GO:0003700; F:transcription factor activity; IEA.
60; GO:0000074; P:regulation of cell cycle; IEA.
60; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 K--GAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAPPRGGAAAATAALDLTGVHILEASSVPPLPE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.9%; Pred. No. 1.6e-46;
Matches 179; Conservative 31; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 420:312-316(2002).
-!- SUBCELLULAR LOCATION: Nuclear (By similar
-!- SIMILARITY: Belongs to the E2F/DP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003316; E2F TDP.
InterPro; IPR009058; Wing hlx DNA bnd.
Pfam; PF02319; E2F TDP; 1.
DNA binding; Nuclear protein; Transcri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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RESULT 3 Q8S182 ID Q8S1 AC Q8S1

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97 LKSMAHIG-----QGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKK 151
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Pfam; Pf02319; Nuclear protein; Transcription; Transcription regulation.
PROTENTIAL 385 AA; 42755 MW; 5DDB4ACA04C52AF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS
                                             DOI=10.1016/S0014-5793(00)02238-9;
                                         MEDLINE=20562805; PubMed=11108847; DOI=10.1016/S0014-5793(00)02238-9
Magyar Z., Atanassova A., de Veylder L., Rombauts S., Inze D.;
"Characterization of two distinct DP-related genes from Arabidopsis
                                                                                                                                                                                                                         GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:00003700; F:transcription factor activity; IEA.
GO; GO:0000074; P:regulation of call cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR003316; E2F_IDP.
InterPro; IPR00358; Wing_hlx_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Populus tremula x Populus tremuloides.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosić
eurosids I; Malpighiales, Salicaceae, Saliceae, Populus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.3%; Score 492; DB 2; Length 385; 47.7%; Pred. No. 5.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Espinoza-Ruiz A., Saxena S., Schmidt J., Mellerowicz E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Espinosa-Ruiz A., Bhalerao R.P.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Transcription factor DP1.
                                                                                                                                               similarity) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 AA.
                                                                                                                       PEBS Lett. 486:79-87(2000).
-!- SUBCELLULAR LOCATION: Nuclear (By-!- SIMILARITY: Belongs to the E2F/DPEMBL; AJ29532; CAC15484.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bhalerao
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                              Q14188; 1CF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=47664;
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SEQUENCE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 LKSMAHIG-----QGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                 Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLUIAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the EZF/DP family.
EMBL; AXO86018; AAM63227.1; -.
HSSP; Q14188; ICF7.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:transcription factor complex; IEA.
GO; GO:0000704; P:transcription factor activity; IEA.
GO; GO:0000707; P:regulation of call cycle; IEA.
InterPro; IPR003316; EZF TDP.
InterPro; IPR003316; EZF TDP.
InterPro; IPR00358; Wing_hlx_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF02319; E2F_TDP, 1.
DNA-binding, Hypothetical protein; Nuclear protein; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation.
SEQUENCE 385 AA; 42826 MW; A4DBDAFBD8F41D1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248
                     01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 PHATVEVEISEDMQLVHFDFNSTPFELHDDNFVLKTMK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.3%; Score 492; DB 2; 47.7%; Pred. No. 5.6e-24;
                                                                                                                                                                                                                                                                                                                                 Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Mismatches
                                                                                Arabidopsis thaliana (Mouse-ear cress).
  Created)
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
  (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                          Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                  annotation
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346 AA; 36907 MW; 53B09A5F68F265B0 CRC64;
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                                                113; Conservative
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                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q14188; 1CF7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                     Similarity
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nes 111;
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   SEQUENCE
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Best Local
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                                                                                                                                                                                                                                                                                DEKNIRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKK 167
                                                                                                                                                                                                                                                                                                                              ALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTSRKARVEIEISDDSKFA 226
                                                                                                                                                                                        22
                                                                                                                                                                                                            SPSSRSEHAMATPASDSTFLRLMHLDIHADDAAT----QDAAANKKKKRGQRAVGADK-- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:0005667; C:transcription factor activity; IEA.
GO; GO:000074; P:transcription of call cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00316; EZF TDP.
InterPro; IPR009058; Wing—llx_DNA_bnd.
Pfam; PF02319; EZF_TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
                          GO; GO:0005667; Citranscription factor complex; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:00000700; F:transcription factor activity; IEA.
GO; GO:00006355; P:regulation of call cycle; IEA.
InterPro; IPR003316; E2F TDP.
InterPro; IPR003058; Wing_hlx_DNA_bnd.
Pfam; PF02319; E2F TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 353 AA; 38444 MW; 33C9F9F440D9DEIF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 APPRGGAAAAATAALDLT-----GVHILEASSVPPLPEAGGNAVQRKG--AVDPDKDR
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gramene; 084VD5; -. GOO 0005634; C:nucleus; IEA. GO; GO:0005667; C:transcription factor complex; IEA. GO; GO:0000767; E:transcription factor activity; IEA. GO; GO:000074; P:regulation of cell cycle; IEA. GO; GO:0006555; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                31;
                                                                                                                                         36.1%; Score 476.5; DB 2; Length 353; 42.7%; Pred. No. 5.1e-23; ive 43; Mismatches 76; Indels 31
                                                                                                                                                  ,1e-23;
os 76; Indels
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
                                                                                                                                                                                                                                                                                                                                                                           HFEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
       EMBL; AF181998; AAQ13675.1;
HSSP; Q14188; ICF7.
                                                                                                                                                      Best_Local Similarity 42.7% Matches 112, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=39947;
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DP TF.
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01-JUN-2003
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                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          48
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GO: GO:0005634; C:nucleus; IEA.

GO: GO:0005634; C:nucleus; IEA.

GO: GO:00056370; C:remacription factor activity; IEA.

GO: GO:000074; P:regulation of cell cycle; IEA.

GO: GO:000074; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR00314; E2F TDP.

InterPro; IPR00314; E2F TDP.

InterPro; IPR00316; E2F TDP; I.

DNA-binding; Nuclear protein; Transcription; Transcription regulation.

SEQUENCE 379 AA; 40893 MW; 913F06C2975FB0CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPRGGAAAAATAALDLTGVHILEASSVPP-----LPEAGGNAVQRKGAVDP-----
                                                                                                                                                                                                                                            MEDLINE=23111120; PubMed=14750518; DOI=10.1023/B:PLAN.000007001.30865.0f; Cooper B., Hutchison D., Park S., Guimil S., Luginbuhl P., Ellero C., Goff S.A., Glazebrook J.; Grazebrook J.; Indentification of rice (Gryza sativa) proteins linked to the cyclin-mediated regulation of the cell cycle."; Plant Mol. Balol. 53:273-279(2003).

-: SUBCELLULAR LOCATION: Nuclear (By similarity).
-: SIMILARITY: Belongs to the E2F/DP family.
EMBL; AX224589; AAO72709.1; -.
                                                                                                                                                      27 APGMOGGGSAATPA-----ASASASTPASETTVARKLDGLDIOGDDAPSSQPATS
                                                                                                                                                                                                             52 RKKEKAAAPRIT-----GWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAHIGOG
                                                                                                                                                                                                                                                                                                                    107 ------PDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVR
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                                                       Gaps
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                    47;
DB 2; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVRRNSIGRAGR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 ATVEVEISEDMQLVHFDFNSTPFELHDDSFVLK----ALGFSGK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                         2 APPRGGAAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVD--
                                                    44; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01.-UUN-2003 (TrEMBLrel. 24, Created)
01.-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01.MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.4%; Score 466.5; DB 2;
37.8%; Pred. No. 2.5e-22;
tive 43; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
  35.7%; Score 471.5; DB 2 39.6%; Pred. No. 1.1e-22;
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154 EVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAEN-VNGIRLPFVLVKTSRK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 MAHIGQ-----GFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 MDRNKVMSSVQKKAAFLKELREKVSSLESLMSRNQEMVVKTQGPAEGFTLPFILLETNPH 202
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.M., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 IKQNAEKPLNENEYNEKNIRRRYYDALNVFMALDIIARDKKEIRWKGLPITCKKDVEEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA binding; Nuclear protein; Transcription; Transcription regulation. SEQUENCE 288 AA; 32560 MW; ECOAD7DC06EF92B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 VQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKS
                                                                                                                                                                                                                                                           Name=T22Pll_60;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Maignaliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0000074; P:regulation of cell cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR003316; E2F_TDP.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.5%; Score 428.5; DB 2 41.3%; Pred. No. 5.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 ARVEIEISDDSKFAHFEFNGAPFTLHDDLSILE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 AVVEIEISEDMQLVHLDFNSTPFSVHDDAYILK 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Mismatches
                                                                                                                                                               288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292
                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9FNY3;
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Cres
01-OCT-2000 (TrEMBLrel. 15, Last
01-MAR-2004 (TrEMBLrel. 26, Last
DP-2 transcription factor-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 41.3
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02319; E2F_TDP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; T48268; T48268.
HSSP; Q14188; 1CF7
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314 VLKTMK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                  243 ILEGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Q9FNY3
ID Q9FNY
AC Q9FNY
DT 01-MA
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                          RLNDLDIHGDDAPSSQAPTSKKKKRGARAVGPDKGGRGLRQFSMKVCEKVESKGRTTYNE 146
                                                                                               206
                                                                                                                           MGLSNYRYBKIKKLEEVRKELV---NKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAE 195
                                                                                                                                                 207 KGLPR---TSINDIBDLQTBLVGLKSRIEKKNTYLQELQDQFVGMQKLIQRNEQLYGSG- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LQNI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 GDDAGSQGASGVKKKKRGQRAAGPDKTGRGLRQFSMKGLISFSAPIMLSSKCLSICEKVE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AKGRITYNEVADEIYSELKSMAHIG-----OGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 KLRNQTLESSAENVN-GIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLS 242
                                                             VADEIYSELKSMAHI-------GQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRW
                                                                                ---DKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02119; E2F_TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                           NV--NGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGV 247
                                                                                                                                                                                                            ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0000074; P:regulation of cell cycle; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weizenegger T., Bancroft I., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

BU Arabidopsis sequencing project;
BU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the E2F/DP family.
-!- SIMILARITY: T48843, 148864.
--- PIR; 148364; 148364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
34.6%; Score 456; DB 2;
Best Local Similarity 41.9%; Pred. No. 1.3e-21;
Matches 103; Conservative 41; Mismatches 68;
                                                                                                                                                                                                                                                                                                           Z
                                                                                                                                                                                                                                                                                                          413
                                                                                                                                                                                                                                                                                                                                                                                                      Name=F12E4 160;
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR003316, E2F TDP.
InterPro, IPR009058; Wing hlx_DNA_bnd.
Pfam; PF02319; E2F_TDP; 1.
                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                     Transcription factor-like protein.
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                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000
                               87
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 43
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| IKQNAEKPLNENEYNEKNIRRRYYDALNVFWALDIIARDKKEIRWKGLPITCKKUVEEVK 146
                                                                            154 EVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAEN-VNGIRLPFVLVKTSRK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                        05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Transcription factor Dp-2 (E2F dimerization partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.3%; Score 399.5; DB 2
37.3%; Pred. No. 5.5e-18;
                                                                                                                                                                                213 ARVEIEISDDSKFAHFEFNGAPFTLHDDLSILE 245
                                                                                                                                                                                                       207 AVVEIEISEDMQLVHLDFNSTPFSVHDDAXILK 239
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                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalla; Eutheria; Primates; NCBI TaxID=9606;
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MSFGLESGKCSL 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=TFDP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                        Q6R754
Q6R754;
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Matches
                                                                                                                                                                                                                                                                                                       RESULT 12
Q6R754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 VRRKLIVDDDSEIGSEKKGQSRTSGGGLRQFSVMVCQKLEAKKITTYKEVADEIISDFAT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., A Kim C.J., Chan G.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., A Palm C.J., Quach H.L., Sakurai T., Satcu M., Southwick A., A Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (MAR-2003) to the EMBL/Genbank/DDBJ databases.

I. Submitted (MAR-2003) to the EMPL/Genbank/DDBJ databases.

I. Submitted (MAR-2013) to the EMPL/Genbank/DDBJ databases.

I. Submitted (MAR-2013) to the EMPL/DP family.

REMBL, AJ294531; CAC15483.1; -.

REMBL, AK117135; BAC41813.1; -.

REMBL, BT005286; AA063350.1; -.
                                                                                                                                                                                                                                                                                                       MEDLINE=20562805; Pubmed=11108847; DOI=10.1016/S0014-5793(00)02238-9; Magyar Z., Atanassova A., de Veylder L., Rombauts S., Inze D.; "Characterization of two distinct DP-related genes from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J., Hayashizaki Y., Shinozaki K.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0005634; C:nucleus; IEA.
GO:0005667; C:transcription factor complex; IEA.
GO:0016874; F:ligase activity; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO:0000074; P:regulation of cell cycle; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                      05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
DP-like protein (EC 6.3.2.19) (E2F dimerisation partner protein)
(DP2a) (Putalive DP-2 transcription factor) (At5g02470).
Name=dpa; Synonyms-At5g02470/722P11 (60, dp2a;
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bergounioux C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation.
SEQUENCE 292 AA; 33038 MW; 644324E13561FEC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding, Ligase; Nuclear protein; Transcription;
                 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.5%; Score 428.5; DB 2
41.3%; Pred. No. 5.3e-20;
iive 49; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; U., GO; GO: 001.

DR GO; GO: 0003700; ...

DR GO; GO: 0004842; F: Ubl.,

DR GO; GO: 0006355; P: regulation of U.

DR GO; GO: 006555; P: regulation of U.

THEFPEO; IPRO0316; E2F_TDP.

THEFPEO; IPRO09068; Wing hix DNA_bnd.

PRO2319; E2F_TDP; 1.

Ligase; Nuclear protein; T.

"""138 MW; 644324
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nes 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rossignol P.;
Submitted (JAN-2002)
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                                                                                                                                                                                                                                        NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                            thaliana.";
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                      SOW WE WANT THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPO
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134 KEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 NQGPPALNSTIQLPPIIINTSRKTVIDCSISSD-KFEYLFNFDNT-FEIHDDIEVLKRMG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 VEAKGRITYNEVADEIYSELKS----MAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                194 AENV----NGIRLPFVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 LTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                          SEQUENCE FROM N.A.
Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
Livingston R.J., Rieder M.J., Poel C.L., Chambers S.W., Schackwitz W.S.,
Nguyen C.P., Nguyen D.A., Poel C.L., Linthauser B.J., Nickerson D.A.;
Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Event=Alternative splicing; Named isoforms=4;
                                                                                                                     partner of
    195 ENV----NGIRLPFVLVKTSRKARVEIBISDDSKFAH-FEFNGAPFTLHDDLSILEGVRR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEAKGRTTYNEVADEIYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSA 194
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                                                                                                                                                                                                                                                                18 LIGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM DELTA), AND CHARACTERIZATION. MEDLINE-95257935; PubMed=7739537; Wu C.L., Zukerberg L.R., Ngwu C., Harlow E., Lees J.A.; "In vivo association of E2F and DP family proteins."; Mol. Cell. Biol. 15:2536-2546(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDP2_HUMAN STANDARD; PRT; 446 AA. Q14188; Q13331; Q14187; Q8WUB8; L5-JUL-1998 (Rel. 36, Created) 30-MAY-2000 (Rel. 36, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Transcription factor Dp-2 (E2F dimerization partner 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 AA; 40230 MW; 8CB52F760F027A8A CRC64;
                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.9%; Score 394;
                                                                          Hypothetical protein DKFZp434G222.
                                  (TrEMBLrel. 13, (TrEMBLrel. 26,
                  01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                  The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=TFDP2; Synonyms=DP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 37.5 es 94; Conservative
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234 SFGLESGKCSL 244
                                                        01-MAR-2004 (TrEMBLrel
                                                                                               Name=DKFZp434G222;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                         NCBI_TaxID=9606;
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                                    01-MAY-2000
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ID TDP2 HUMAN

DT 15-4UE,

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A Straubberg R.L., Feingold E.A., Grouez L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,

Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleron M., Soarsa M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malak J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahe J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Schwultz J., Miyers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang Y., Chellappan S.P.; "Transcription of DP transcription factors "Transcriptional activation and expression of DP transcription factors during cell cycle and TPA-induced U937 differentiation."; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96353862; PubMed=875520; DOI=10.1073/pnas.93.15.7594; Rogers K.T., Higgins P.D.R., Milla M.M., Phillips R.S., Horowitz J.M.; "DP-2, a heterodimeric partner of E2F: identification and characterization of DP-2 proteins expressed in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 62-79 FROM N.A. (ISOFORM DELTA), AND ALTERNATIVE SPLICING
                                                                                        Zhang Y., Chellappan S.P.; "Cloning and characterization of human DP2, a novel dimerization
                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterization of DP-2 proteins expressed in vivo.";
Proc. Natl. Acad. Sci. U.S.A. 93:7594-7599(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-102 FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM GAMMA).
SEQUENCE FROM N.A. (ISOFORM DELTA)
                             TISSUE=Kidney;
MEDLINE=95303470; PubMed=7784053;
                                                                                                                                                                              Oncogene 10:2085-2093 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
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204
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         SEQUENCE
                           Query Match
                                      Local
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                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                          Name=Delfa; Synonyms=48 kDa;
IsoId=Q14188-4; Sequence=VSP 001352;
IsSUE SPECIFICITY: High levels in heart and skeletal muscle. Also found in placenta, kidney, brain, lung and liver. The presence as well as the abundance of the different transcripts appear to vary significantly in different tissues and cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform Beta, isoform Gamma and isoform Delta).
                                                                 IsoId=Q14188-3; Sequence=VSP_001352, VSP_001353, VSP_001354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphoserine (by CDK2) (Potential). Phosphoserine (by CDK2) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VSP_001352.
Missing (In isoform Beta and isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asp/Glu-rich (acidic) (NCB domain)
Comment=Additional isoforms seem to exist. Experimental
                                                                                                                                                                                                                                                                                                                                                                            Nuclear localization signal (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> SQ (in isoform Gamma)
                                                                                                                                                                                                                                                                                                                                        GO; GO:0003677; F:DNA binding; TAS.
GO; GO:0003712; F:!transcription cofactor activity; TAS.
InterPro; IPR003136; E2F TDP.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
                  Name=Alpha; Synonýms=49 kDa;
IsoId=Q14188-1; Sequence=Displayed;
Name=Beta; Synonyms=43 kDa;
IsoId=Q14188-2; Sequence=VSP_001352, VSP_001353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dimerization (Potential)
            confirmation may be lacking for some isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTId=VSP_001354.
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/FTId=VAR_002272
                                                                                                                                 PTM: Phosphorylated.
SIMILARITY: Belongs to the E2F/DP family.
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EMBL, U1842; AAB6038.1; --
EMBL, BC021113; AAR13113.1; --
EMBL, U75488; AAB37321.1; --
EMBL, U35117, AAC5642.1; --
PDB; 1CF7; X-ray, B-121-215.
TRANSFAC; T03000; --
                                                                                                                                                                                                                                                                                                    Genew; HGNC:11751; TFDP2.
H-InvDB; HIX0003733; -.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSA 194
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 28, Last sequence update)
01-MAR-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:4732486C09 product:transcription factor Dp 2, full
insert sequence (Mus musculus 16 days embryo lung cDNA, RIKEN full-
length enriched library, clone:8430403A04 product:transcription factor
Dp 2, full insert sequence).
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length GNRAs.";
Nature 420:563-573 (2002).
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SECUENCE FROM N.A.
STRANIE-C79BL/GJ; TISSUE=Lung, and Skin;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/GF.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                 78 VEAKGRITYNEVADEIYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAKEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENV ----NGIRLPFVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVRR
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                                                                                                                                                                                                             18 LIGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                   Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                   16;
                                                                                      Length 446;
                                                                                                                                                89; Indels
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
206
49236 MW; 19A6C85BAD61DFF1 CRC64;
                                                                                29.9%; Score 394; DB 1; 37.5%; Pred. No. 1.5e-17; ive 52; Mismatches 89
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321 SFGLESGKCSL 331
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                                446 AA;
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C STRAIN-657BL/61, TISSUB-Lung, and Skin;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Aruda S., Furuno M., Hanagaki T., Haraoka T., Hirozane T.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
C -- Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
C -- Submitted (UL-2001) to the EMBL/GenBank/DDBJ databases.
C -- Submitted (UL-2001) to the EMBL/GenBank/DDBJ databases.
C -- Submitted (UL-2001) to the EZF/DP family.
C -- SIMLAKITY: Belongs to the EZF/DP family.
C -- SIMLIARITY: Belongs to the EZF/DP family.
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MGD; MG1:2442257; A330800J22Rik.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005667; C:transcription factor activity; IEA.

GO; GO:0003074; P:regulation of call cycle; IEA.

GO; GO:000074; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR00316; B:ZP TDP.

InterPro; IPR009058; Wing_hlx_DNA_bnd,

Fam; PF02319; EZF TDP; 1.

DNA-binding; Nuclear protein; Transcription; Transcription regulation.

SEQUENCE 385 AA; 42846 MW; ZFCOFE85D8ACE220 CRC64;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                    Query Match 29.8%; Score 393; DB 2; Length 385; Best Local Similarity 39.0%; Pred. No. 1.4e-17; Matches 99; Conservative 47; Mismatches 86; Indels 2
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TOPOLOGY:
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US-08-723-415B-6
Sequence 2, Appli
Sequence 9220, Ap
Sequence 4, Appli
Sequence 4, Appli
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Sequence 10, Appl
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Sequence 1056, Ap
Sequence 10, Appl
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Sequence 1031, Ap
                                                                                               February 4, 2005, 20:22:24; Search time 43 Seconds (without alignments) 453.102 Million cell updates/sec
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                                                                                                                                                             US-10-088-830-2
1319
1 MAPPRGGAAAAATAALDLTG.....SILEGVRRNSIGRAGRATLH 261
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Sequence 2,
Sequence 2,
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Sequence 11
Sequence 2,
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Sequence 1
Sequence 1
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/cgn2_6/prodata/1/iaa/5B_COMB.pep:*
/cgn2_6/prodata/1/iaa/6A_COMB.pep:*
/cgn2_6/prodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-189-627A-6
US-09-10-861A-6
US-09-110-861-8
US-09-110-861-8
US-09-110-861-8
US-08-723-415B-2
US-09-189-627A-2
US-09-189-627A-2
US-09-189-627A-4
US-09-189-627A-4
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US-09-111-2
US-08-723-415B-11
US-08-723-415B-11
US-08-131-2
US-09-10-861-2
US-09-10-861-2
US-09-10-861-11
US-09-10-861-11
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Maximum Match 100%
Listing first 45 summaries
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14, Appli
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APPLICANT: LaThangue, Nicholas B.
APPLICANT: delaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORRENT APPLICATION NUMBER: 25,327
REGISTRATION NUMBER: 25,327
TELECOMMUTCATION INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
TELECOMMUTCATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-462-174-2
US-09-248-796A-21863
US-09-640-211A-1167
                                                                                                                                                                 US-08-723-415B-13
US-08-481-814A-6
US-08-801-02-1
US-09-189-627A-13
US-09-242-737-2
US-09-215-113-1
US-09-710-861-13
US-08-139-937-14
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US-07-882-711-2
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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us-10-088-830-2.rai

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; TYPE: PRT
; ORGANISM: mouse
US-09-710-861-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 VEAKGRITYNBVADEIYSELKS----MAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEK 133
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                              78 VEAKGRITYNEVADEIYSELKS----MAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEK 133
                                               134 KEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESS 193
                                                                                                        194 AEN---VNG-IRLPFVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                                                   ---NGKGLRHFSMKVCEK 65
                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09189627A
; Sequence 6, Application US/09189627A
; Patent No. 619504
; GENERAL INFORMATION:
    APPLICANT: La Thangue, Nicholas
; APPLICANT: La Thangue, Nicholas
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
; TILE REFERENCE: 620-54
; CURRENT PAPLICATION NUMBER: US/09/189,627A
; CURRENT PILING DATE: 1996-09-11-10
; PRIOR PPLICATION NUMBER: 08/723,415
; PRIOR PPLICATION NUMBER: 08/723,415
; PRIOR FILING DATE: 1996-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 LTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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 28 VTQTHIAEAA-------GWVPSKRSKKGDK-
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; Sequence 6, Application US/09710861
; Patent No. 6387649
; Patent No. Garnarion:
; APPLICANT: La Thangue, Nicholas
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Best Local Similarity
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78 VEAKGRITYNEVADEIYSELKS----MAHIGOGFDEKNIRRRVYDAFNVLIALRVIAKEK 133
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APPLICANT: de la Luna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
CURRENT APPLICATION NUMBER: US/09/110,861
CURRENT APPLICATION NUMBER: US/09/110,861
CURRENT FILING DATE: 1908-11-13
PRIOR APPLICATION NUMBER: US/09/189,627
PRIOR APPLICATION NUMBER: US/09/189,627
PRIOR APPLICATION NUMBER: US/09/189,627
PRIOR FILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-05-16
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 6:
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; Sequence 8, Application US/08723415B
; Patent No. 5859199
; GENERAL INFORMATION:
    APPLICANT: LaThangue, Nicholas B.
    APPLICANT: LaThangue, Nicholas B.
    APPLICANT: ALTHANGUE, NICHOLAS B.
    TITLE OF INVENTION: THEREOF
    NUMBER OF SEQUENCES: 2.
    CORRESPONDENCE ADDRESS: 2.
    ADDRESSEE: NIXON & VANDERHYE P.C.
    STREET: 1100 No. 5859199th Glebe Rd. 8th floor
    CITY: ALLINGTON
    STREET: VANDERESS: 2.
    STREET: VANDERESS: 2.
    STREET: 100 No. 5859199th Glebe Rd. 8th floor
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ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
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37.3%; Pred. No. 4.7e-29;
tive 51; Mismatches 74;
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244 MSFGLESGKCSL 255
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132 EKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLE 191
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79 CEKVORKGITSYNEVADELVSEFINSNNHLAADSAYDQENIRRRVYDALNVLMAMNIISK 138
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APPLICANT: La Thangue, Nicholas

APPLICANT: La Thangue, Nicholas

ITILE OF INFORMATION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF

TITLE OF INFORMATION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF

FILE REFERENCE: 620-54

CURRENT APPLICATION NUMBER: US/09/110,861

PRIOR FILING DATE: 1996-11-13

PRIOR APPLICATION NUMBER: 08/723,415

PRIOR PILING DATE: 1996-09-30

PRIOR PILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-05-15

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTIN VOY: 2.0
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APPLICANT: LaThangue, Nicholas B.
APPLICANT: deLaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
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Patent No. 6387649
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257 MGMSFGLESGKCSL 270
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Best Local Similarity 38.6<sup>§</sup>
Matches 98; Conservative
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APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Susana
ITILE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 620-54
CURRENT APPLICATION WIMBER: Us/09/189,627A
CURRENT FILING DATE: 1996-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR PILING DATE: 1996-05-15
PRIOR FILING DATE: 1996-05-15
PRIOR FILING DATE: 1996-05-15
PRIOR FILING DATE: 1996-05-15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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                         NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-189-627A-8
; Sequence 8, Application US/09189627A
; Patent No. 6159691
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            : 385 amino acids
amino acid
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Best Local Similarity 38.67
Matches 98; Conservative
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Best Local Similarity
Matches 98; Conserv
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셤 ò 셤 Š ద ò 셤 ઠે 원 10;

Gaps

22;

Length 446; 86; Indels

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89 VTQTHIAEA-----AGWVPSSRKRAREFIDSDFSESKRSKKGDK-NGKGLRHFSMKV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 EKKEIKWIGLPTNSAQECQNLEIEKQRRIERIKQKRAQLQELLLQQIAFKNLVQRNRQNE 259
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Sequence 2, Application US/09710861

Patent No. 6387649

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas

APPLICANT: de 1a Luna, Susana

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF

FILE REPERENCE: 620-54

CURRENT APPLICATION NUMBER: US/09/180, 627

PRIOR APPLICATION NUMBER: US/09/189, 627

PRIOR APPLICATION NUMBER: US/09/189, 627

PRIOR APPLICATION NUMBER: US/09/189, 627

PRIOR APPLICATION NUMBER: US/09/189, 627

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PRIOR APPLICATION NUMBER: US/09/189, 627

PRIOR APPLICATION NUMBER: US/09/189, 627

PRIOR APPLICATION NUMBER: US/09/189, 627

PRIOR APPLICATION NUMBER: US/09/189, 627

PRIOR APPLICATION UMBER:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

29.5%; Score 389; DB 3; Length 446;
Best Local Similarity 38.6%; Pred. No. 6.9e-29;
Matches 98; Conservative 48; Mismatches 86; Indels 3
                                                                                                                                                                                                                                                                                                                                              29.5%; Score 389; DB 3; 38.6%; Pred. No. 6.9e-29; tive 48; Mismatches 86,
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 961
PRIOR FILING DATE: 1996-05-15
PRIOR FILING DATE: 1996-05-15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 VRRNSIGRAGRATL 260
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                                                                                                                                                                                                                                                                                                                                                                                                                   98; Conservative
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 98; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: mouse US-09-710-861-2
                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: mouse
US-09-189-627A-2
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Sequence 2, Application US/09189627A;
Patent No. 6159691
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana;
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF;
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A;
CURRENT PILING DATE: 1938-11-10;
PRIOR APPLICATION NUMBER: 08/723,415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                     COMPUTER SEADABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPOTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTWARE: PETCHION DATA:

APPLICATION NUMBER: US/08/723,415B

FLING DATE: 30-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9610195.1

FLING DATE: 15-MAY-1996

ATTCRNEY/AGENT INFORMATION:

NAME: CTAWFORM, ARTHUR R.

REGISTRATION NUMBER: 25,327

REGISTROCE/DOCKET NUMBER: 117-220

TELECOMMUNICATION INFORMATION:

TELEFERK: 703-816-4100

TELEFERK: 703-816-4100
                                          NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: ULXON & VANDERHYE F.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
             HILE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 MGMSFGLESGKCSL 331
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                      CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                        COUNTRY:
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22; Gaps

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78 VEAKGRTTYNEVADEIYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 EIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 VTQTHIABAA-----GWVPSKRSKKGDK-----NGKGLRHFSMKVCEK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09189627A

Sequence 4, Application US/09189627A

Sequence 4, Application US/09189627A

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas

APPLICANT: de la Luna, Susana

TITLE OF INVENTION: TRANSCRIPTION PACTOR DP-3 AND ISOFORMS THEREOF

FILE REFERENCE: 620-54

CURRENT APPLICATION NUMBER: US/09/189,627A

CURRENT FILING DATE: 1998-11-10

FRIOR APPLICATION NUMBER: 08/723,415

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-15

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATCHIN Ver. 2.0

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.1%; Score 384; DB 2; Length 369; 37.5%; Pred. No. 1.6e-28; tive 50; Mismatches 75; Indels
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             25,327
                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFRENCE/DOCKET NUMBER: 117-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPE: amino acida TOPOLOGY: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
                      COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 37.5
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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244 SFGLESGKCSL 254
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                           192 SSAEN----VNG-IRLPFVLVKTSRKARVEIEISDDSKFAH-FBFNGAPFTLHDDLSILEG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLE 191
                                                                                                                         260 QQNGGPPAVNSTIQLPFIIINTSRKTVIDCSISSD-KFEYLFNFDNT-FEIHDDIEVLKR 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 DEIYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 KIKKLEEVRKELVNKIRNKKALLOEIEKOFDDLONIKLRNOTLESSAENV----NGIRLP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 FVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVRRNSIGRAGRATL 260
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Patent No. 5859199
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: deLaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ANDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.2%; Score 385; DB 4; Length 331; 38.7%; Pred. No. 1.1e-28; Live 48; Mismatches 84; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CLOOL307;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PERESEQ for Windows Version 4.0
                                                                                                                                                                                        247 VRRNSIGRAGRATL 260
                                                                                                                                                                                                                                      318 MGMSFGLESGKCSL 331
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-949-016-9220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-9220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 9220
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US-08-723-415B-4
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222 DSKFAH-FEFNGAPFTLHDDLSILE 245
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D-KFEYLFNFDNT-FEIHDDIEVLK 301
                                                                                                                     RESULT 14
10S-08-723-415B-11
1 Sequence 11, Application US/08723415B
2 Patent No. 5859199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crawford, Arthur R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 amino acids
                            250 NSIGRAGRATL 260
                                                 : :|: :|
244 SFGLESGKCSL 254
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-723-415B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                           GENERAL INFORMATION:
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CITY: A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EN----VNG-IRLPFVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVRR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 VEAKGRITYNEVADEIYSEL-KSMAHIG--OGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLOEIEKOFDDLONIKLRNQTLESSA 194
                                                                                                                                                                                                                                                                                                                           78 VEAKGRITYNEVADEIYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
                                                                                                                                                                                                                                                 EIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSA 194
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                                                                                                                                                                                 28 VIQTHIAEAA------GWVPSKRSKKGDK-----NGKGLRHFSMKVCEK 65
                                                                                                                                                           18 LIGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Nicholas
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
TILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/710,861
CURRENT FILING DATE: 2000-11-13
PRIOR PELING DATE: 1998-10-10
PRIOR PELING DATE: 1998-10-10
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR PELING DATE: 1996-09-30
PRIOR FILING DATE: 1996-09-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 369
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                                                                                     29.1%; Score 384; DB 3; Length 369; 37.5%; Pred. No. 1.6e-28;
                                                                                                                          50; Mismatches
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US-09-710-861-4
; Sequence 4, Application US/09710861
; Patent No. 6387649
                                                                                                                          94; Conservative
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Best Local Similarity
Matches 94; Conserva
                                                                                     Query Match
Best Local Similarity
Matches 94; Conserv
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ORGANISM: mouse
LENGTH: 369
TYPE: PRT
ORGANISM: mouse
                                         ; ORGANISM: mov
US-09-189-627A-4
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50 KDRKKEKAAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
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186 QGPPAVNSTIQLPFIIINTSRKTVIDCSISSD-KPEYLFNFDNT-FEIHDDIEVLKRMGM 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEISD
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LaThangue, Nicholas B.
APPLICANT: detaluna, Susana
IITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: REALBLE FORDY disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
28.7%; Score 378.5; DB 2;
Best Local Similarity 42.4%; Pred. No. 6.2e-28;
Matches 87; Conservative 41; Mismatches 60;
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50 KDRKKEKAAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
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US-08-428-131-2

Sequence 2, Application US/08428131

Patent No. 5863757

GENERAL INFORMATION:

RAPLICANT: La Thangue, Nicholas Barrie

TITLE OF INVENTION: Transcription Factor DP-1

WUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon & Vanderhye

STREET: 1100 No. 5863757th Glebe Road, 8th Floor

CITY: Arlington
STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC. Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

MAPLICATION NUMBER: US/08/428,131

FILING DATE: 23-JUN-1995

CURSSIFICATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 125,327

REFERENCE/DOCKET NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 17-181

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFROME (703) 816-4100

INFORMATION POR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 410 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: And ALLINGARES ACID NO: 2.
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Job time : 44 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 D-KFEYLFNFDNT-FEIHDDIEVLK 301
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644.003 Million cell updates/sec
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1319
1 MAPPRGGAAAAATAALDLTG......SILEGVRNSIGRAGRATLH 261
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/ (gn2_6/ptodatea/2/pubpaa/USO6_NEW_PUB.pep:*
/ (gn2_6/ptodatea/2/pubpaa/USO6_PUBCOMB.pep:*
/ (gn2_6/ptodatea/2/pubpaa/USO6_PUBCOMB.pep:*
/ (gn2_6/ptodatea/2/pubpaa/USO8_NEW_PUB.pep:*
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/ (gn2_6/ptodatea/2/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 234773, Sequence 10, Appl Sequence 166159, Sequence 1, Appli Sequence 46532, A	Sequence 43, Appl Sequence 52434, A Sequence 435, App Sequence 257840, Sequence 248849,		Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 8, Appli Sequence 6, Appli	Sequence 9, Appli Sequence 13626, A Sequence 71965, A Sequence 25931, Sequence 10, Appl	Sequence 9, Appli Sequence 10, Appli Sequence 10, Appl Sequence 95, Appli Sequence 8, Appli Sequence 2, Appli
		12167	US-10-767-701-43 US-09-842-484A-2 US-09-842-484A-3 US-10-184-485-3 US-10-217-613-3 US-10-217-613-8 US-10-642-248-4	US-09-220-091-9 US-10-369-493- US-10-425-114- US-10-424-599- US-09-879-959-1	4 US-10-011-76BB-9 4 US-10-011-71B-9 4 US-10-172-527-10 4 US-10-326-185-95 5 US-10-309-560-8 6 US-10-642-248-2
	1156 1178 444 123 123	1957 718 397 1317	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		972 972 972 10 10 10 10 10 10 10 10 10 10 10 10 10
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225.5 203.5 150 133	112.5 111.5 111 110.5	108.5 107 106 105	104.5 104.5 104.5 104.5 104.5	103.5 103.5 102.5 101.5	101.5 101.5 101.5 101.5 101.5
14 11 17 11 18	19 20 22 23	4 2 2 2 4 4 2 6 6 4	2 3 3 3 3 5 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		4 4 4 4 4 4 5 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

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APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 136371
LENGTH: 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.8%; Score 842; DB 16; Length 369; 50.4%; Pred. No. 2e-66; cive 32; Mismatches 36; Indels 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT4530_37957C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAPPRGGAAAATAALDLTGVHILEASSVPPLPE----
:-10-437-963-136371
Sequence 136371, Application US/10437963
Publication No. US20040123343A1
                                                                                              APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 50.4
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
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258 KAMK 261
                      RESULT 3
US-10-424-599-186648
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US-10-424-599-185947
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Sceni, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
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APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Scenification Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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61 KKSVSLRSGGGGNAAEREEGGA---NRNGKKEKTGAQRITGWGLREFSKIGFTKLPGPGL 117
                                                                                   | :|||||||||
118 SRPGGKHSYCAEVTAVFTLPYPGGKPGNRGNRAVTGGMVNPGVDCFVSKKVEAKGRTTYN 177
                                                                                                                                         88 E------VADEIYSELKSMAHIGQGFDEKNIRRRVYDAFNVLIALRVI 129
                                                                                                                                                                 130 AKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQT 189
                                                                                                                                                                                                                                         190 LESSAENVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVRR 249
                                                                                                                                                                                                                                                                                                                       298 SQRPAESVNGILLPFILLIKTSRKARVEIEISEDSKFARFDFNGAPFTWHDDVSILEAIRR 357
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                                                               -----VCEKVEAKGRTTYN
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Best Local Similarity 39.9%; Pred. No. 8e-33;
Matches 107; Conservative 45; Mismatches 76; Indels
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US-10-425-114-46555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 SDDSKFAHFEFNGAPFTLHDDLSILEGV 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46555, Application US/10425114 Publication No. US20040034888A1
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US-10-425-114-46555
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Sequence 186648, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53232)8
FILE REPERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 186648
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Zhou Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 RVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIE-KQFDDLQNIKL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Clone ID: PAT_MRT3847_139556C.1.pep
US-10-424-599-186648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(320)
OTHER INFORMATION: unsure at all Xaa locations
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
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ORGANISM: Glycine max
FEATURE:
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ORGANISM: Glycine max
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Sequence 166188, Application US/10437963
; Sequence 166188, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharcov, Andrey A.
; APPLICANT: Boukharcov, Andrey A.
; APPLICANT: Li, Ping
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-65-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166158
                                                                                                                                                                                                                        RESULT 6
US-10-767-701-49206
is Sequence 43206, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
    APPLICANT: ENOU, Yihua
; APPLICANT: Thou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules Thereof For Plant Improvement
; FILE REFERENCE: 38-21 (5535) B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 49206
; LENGTH: 120
                                138 WMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENV 197
  166 KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEISD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 WACL-HFQYEYI-KLESTRKELMIRVKNKKKLLQEIERQFDDLQNIKFRNQLLQRPAESA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 NGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVRRNS 251
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Best Local Similarity 37.7%; Pred. No. 1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: LIB3476-039-P1-K1-D2.pep
US-10-767-701-49206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Clone ID: PAT_MRT4530_64895C.1.pep. US-10-437-963-166158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 28.4%; Score 374; DB 16; Best Local Similarity 67.5%; Pred. No. 2e-25; Matches 77; Conservative 17; Mismatches 18;
                                                                                                                                  285 D-KFEYLFNFDNT-FEIHDDIEVLK 307
                                                                                                     222 DSKFAH-FEFNGAPFTLHDDLSILE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Sorghum bicolor
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Sequence 4846, Application US/10106698

Publication No. US20030109690A1

GENERAL INFORMATION:

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

FILE REPERENCE: PA005P1

CURRENT PILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE PATENTIN Ver. 3.0

SEQ ID NO 4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE LOCATION: (351)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE
LOCATION: (352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC FEATURE LOCATION: (342)
OTHER INPORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 KDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
                                                                                                                                                                                                                                                                             50 KDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAH----IG 104
                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-4846
                                                                                                                                                                                                                                                                                                                                                                                     165 NKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTSRKARVEIEISDDS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.4%; Score 374.5; DB 14; Length 355;
42.0%; Pred. No. 8.1e-25;
tive 42; Mismatches 60; Indels 17; Gaps
                                                                                                                                Gaps
                                                                                                                                9
                                                                          Length 314;
                                                                                                                                66; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_138923C.1.pep
US-10-424-599-185947
                                                                        33.2%; Score 438; DB 15;
45.9%; Pred. No. 1.5e-30;
tive 39; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 KFAHFEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 42.08
Matches 86; Conservative
                                                                                                                             94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-106-698-4846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 VADEIYSELKSMAH----IGQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 ------FDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVR 156
                                                                                                         207
                                                                                                                                                51
                                    27 APGMOGGGSAATPA-----ASASASTPASETTVARRLDGLDIOGDDAPSSOPATS 76
                                                                                                                                     157 KELV---NKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLV----
                 2 APPRGGAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVD------PDKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: LIB3170-045-C12_FLI.pep
US-10-425-114-36974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.4%; Score 361; DB 15;
46.4%; Pred. No. 6.7e-24;
tive 30; Mismatches 53;
Mismatches
                                                                                                                                                                                                                             RESULT 8
US-10-425-114-36974
Sequence 36974, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                             208 ----KTSRKARVEIEIS 220
                                                                                                                                                                                                254 LAKNOMIRKPGLEMEVS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
27.4%;
Best Local Similarity 46.4%;
Matches 77; Conservative 3
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-220-091-7
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 Matches
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Sequence 7, Application US/09220091
Patent No. US20020064523A1
GENERAL INFORMATION:
APPLICANT: H. Robert Horvitz
APPLICANT: Craig Ceol
APPLICANT: Xiaowei Lu

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APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Screan, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT FILING DAINS: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 207

TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYPP: TYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 GLRHFSTKVCEKVKEKGLTNYNEVADELVADYFQNNLIKQIDVVKQEYDMKNIRRRVYDA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 LONIKLRNOTLE---SSAENVNGIRLPFVLVKTSRKARVEIBISDDSKFAHFEFNGAPFT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 GLREYSKIVCEKVEAKGRITYNEVADEIYSE-----LKSMAHIGOGFDEKNIRRRVYDA
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26.0%; Score 342.5; DB 15; Length 207;
Best Local Similarity 44.4%; Pred. No. 2.7e-22;
Matches 75; Conservative 29; Mismatches 48; Indels 17;
TITLE OF INVENTION: A TUMOR SUPPRESSOR PATHWAY IN C. ELECANS FILE REFERENCE: 0.1997/202003
CURRENT APPLICATION NUMBER: US/09/220,091
CURRENT FILING DATE: 1.998-1.2-.3
EARLIER APPLICATION NUMBER: 60/047,996
EARLIER PILING DATE: 1.997-05-28
EARLIER PILING DATE: 1.998-05-28
EARLIER PILING DATE: 1.998-05-28
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.8%; Score 354; DB 9; Length 575; 41.3%; Pred. No. 1e-22; iive 34; Mismatches 67; Indels
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US-10-425-114-71403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-220-091-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.85
Best Local Similarity 41.33
Matches 78; Conservative
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228 IHDDFEILK 236
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51 DRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAHIG----QG 106
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                                                                                                                                                                                                                                                                                                   167 KALLQEIEKQFDDLQNIKLRNQTLESSAEN----VNGIRLPFVLVKTSRKARVEIEISDD 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 DRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAHIG----QG 106
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                                                                                                                             Gaps
                                                                                                                          15;
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                                                                          DB 14; Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.7%; Score 299.5; DB 16; Length 405; Best Local Similarity 33.7%; Pred. No. 4.6e-18; Matches 68; Conservative 47; Mismatches 72; Indels 15;
                                                                       22.7%; Score 299.5; DB 14; Length 33.7%; Pred. No. 4.6e-18; tive 47; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-345-837-24

Sequence 24, Application US/10345837

Publication No. US20040137440A1

GENERAL INFORMATION:

APPLICANT: Lin, Biaoyang

TITLE OF INVENTION: Androgen Regulated Nucleic Acid

TITLE OF INVENTION: Androgen Regulated Nucleic Acid

TITLE OF INVENTION: Molecules and Encoded Proteins

FILE REFERENCE: P-IS 5589

CURRENT APPLICATION NUMBER: US/10/345,837

CURRENT FILING DATE: 2003-01-15

PRIOR FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 SKFAHFEFNGAPFTLHDDLSIL 244
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275 KSEYLFKFNSS-FEIHDDTEVL 295
                                                                                                                        68; Conservative
; ORGANISM: Homo sapiens
US-10-053-248-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-345-837-24
                                                                       Query Match
Best Local Similarity
Matches 68; Conserval
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-2163221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 RINDLDIHGDDAPSSQAPTSKKKKRGARAVGPDKGGRGLRQFSMKVCEKVESKGRTTYNE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 ------QQYDEKNIRRRVYDALNVIMAMEIISKDKKEIQWKGLPR---TS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 INDIEDLQTELVGLKSRIEKKNTYLQELQDQFVGMQKLIQRNEQLYGSG-NIPSGGVALP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 VADEIYSELKSMAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEK 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 PPSGGAQSASTSG-----GSAGSPSSRSEQHVPAAAGMAAGAAASTPISENTFL
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                            ----RNSIGRAGRAT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.6%; Score 337.5; DB 16; Length 263; Best Local Similarity 35.5%; Pred. No. 1.1e-21; Matches 97; Conservative 33; Mismatches 56; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/10053248
Publication No. US2003014418841
GENERAL INFORMATION:
APPLICANT: Lin, Biaoyang
TITLE OF INVENTION: Molecules and Encoded Proteins
FILE REPERENCE: P. IS 4814
CURRENT APPLICATION WHREE; US/10/053,248
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 24
LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_65721C.1.pep
US-10-437-963-167076
221 DDSKFAHFEFNGAPFTLHDDLSILEGVR-
                                                                                                                                                                   Sequence 167076, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Ebou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Oryza sativa
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US-10-053-248-24
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61 RITGWGLREYSKIVCEKVEAKGRITYNEVADEIYSELKSMAH----IGQGFDEKNIRRR 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
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Best Local Similarity 39.9%; Pred. No. 5.2e-12;
Matches 55; Conservative 20; Mismatches 40; Indels 23;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FLING DATE: 08 - Aug - 2002
CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                  FEATURE:

, OTHER INFORMATION: Clone ID: PAT_MRT3847_54029C.1.pep

US-10-424-599-234773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/10214188
; Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANUE, NICHOLAS B.
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATJOANDA: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
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148 VYDALNVLMAMDIISKDK 165
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                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
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US-10-214-188-10
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74 VCEKVEAKGRITYNEVADELYSELKSM-AHI---GQGFDEKNIRRRVYDAFNVLIALRVI 129
                                                                                                                                                                                                                                                                         5; Gaps
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                                                                                                                                                                Query Match
15.4%; Score 203.5; DB 14; Length
Best Local Similarity 58.3%; Pred. No. 1.6e-10;
Matches 42; Conservative 13; Mismatches 12; Indels
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-214-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: February 4, 2005, 20:45:29 Job time : 134 secs
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63 SKEKKEIKWIGL 74
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OM protein

Run on:

Sequence:

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                              AY224551 Oryza sat
AX224551 Oryza sat
AX449314 Sequence
BY005286 Arabidops
AX1319027 Arabidops
AX449329 Sequence
AX112307 Arabidops
AX449329 Sequence
AX712207 Sequence
AX712207 Sequence
AX712207 Sequence
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AX712207 Sequence
AX734251 Sequence
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AX120688 Sequence
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AX120689 Sequence
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                      Populus t
Populus t
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AR029043 Sequence
AR120686 Sequence
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AX003677 Sequence
A67522 Sequence 3
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Gutierrez-Armenta,C.C. and Ramirez-Parra,E.C.
Gutiert dp proteins and uses thereof
Patent: WO 0121644-A 1 29-MAR-2001;
CONSEJO SUPERROR DE INVESTIGACIONES CIENTIFICAS (ES)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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ATH319027
AX449297
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AR029045
AR120688
AR210078
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AY224589
AX449342
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AR380911
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СО489116
СО494960
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Triticum monococcum
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AX100704
LOCUS
DEFINITION
ACCESSION
VERSION
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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AJ271917 Triticum
AY224529 Oryza sat
AK111611 Oryza sat
                                                                          6, 2005, 20:16:37 ; Search time 4657 Seconds (without alignments) 2715.656 Million cell updates/sec
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                                                                                                                                               1 MAPPRGGAAAATAALDLTG......SILEGVRRNSIGRAGRATLH 261
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                    - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                         4708233 segs, 24227607955 residues
                                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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TSP271917
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Maximum DB seq length: 200000000
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99 htg: **
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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98.9
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1304
890.5
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Jatabase :

Total number

Searched:

Score

Result No.

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Scores
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DEFINITION
                                                                          ORGANISM
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                              ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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AVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADBIYSELKSMAH
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                                                                                                                                                                                                                                                             GlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAlaAlaAlaPro
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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Gutierrez,C.
Direct Submission
Submitted (03-FEB-2000) Gutierrez C., C.S.I.C.-U.A.M.,
Biologia Molecular, Cantoblanco, Madrid 28049, SPAIN
Location/Qualifiers
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/gene="dp"
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DP gene; E2F dimerization partner
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/note="derived from yeast two-hybrid experiments"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsnGlyIle
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Ellero, C., Goff, S. and Glazebrook, J.
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Yokomizo, S. and Yoshimura, A.  TITLE Rice full-length cDNA JOURNAL Unpublished REFERENCE 3 (bases 1 to 1174) AUTHORS Kikuchi, S.  TITLE Direct Submitsed (12-SEP-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007) Fax:81-29-838-7007) COMMENT This clone is one of the 32K full-length cDNA clones from japonica rice. URL: http://cdna01.dna.affrc.go.jp/cDNA/ NIAS Rice Full-Length CDNA Project Team: Kikuchi, S., Satoh, K.,	Nagata, T., Kawagashira, N., Milmoro, N., Talandero, N., Talandero, N., Talandero, N., Talandero, N., Tandada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, N. and Nakahama, Y. FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusunegi, T., Lu, M., Masuda, H., Miura, J., Mizune, Y., Kusunegi, T., Lu, M., Kyu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, O., Yokomizo, S., Yoshimura, M., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Haraoka, T., Arakawa, T., Carninci, P., Fukuda, S., Haramoto, K., Haraoka, T., Harakwa, T., Carninci, P., Fukuda, S., Haramoto, K., Haraoka, T., Harakwa, T., Kanagawa, S., Kanch, H., Kouda, M., Kanagawa, I., Kanagawa, S., Kanono, H., Kouda, M., Koyaka, Hirozane, T., Natina, W., Muyazaki, A., Murata, M., Koyaka, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,	ORAGUNE, N. ANGHILA, K., NUMBERAKI, K., ORBONIA, K., SAKARURARATEA, N., SAKATURE, N., SAKATURE, N., SAKATURE, N., SAKATURE, N., SAKATURE, N., SAKATURE, N., SAKATURE, N., SAKATURE, N., SAKATURE, N., SAKATURE, N., TAGARI, K., TAGARI, K., TAGARI, M., TAGARI, TAGARI, TAGARI, T., TAGARAH, N., TAGARI, M., TAGARI, M., TAGARI, M., A and Hayashizak, Y. Tomaru, A., Tagari, M., Toya, T., Waki, K., Tagari, Tagari, A., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Tagari, Tagari, A., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Tagari, Tagari, M., Tagari, M., Toya, T., Waki, K., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M., Tagari, M.,	
184 LysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsnGlyIleArgLeuPro 203	AKIL1611  AKIL1611  AKIL1611  DOCUS  DEFINITION OFTZA SALIVA (japonica cultivar-group) cDNA clone:J013105118, full insert sequence.  ACCESSION AKIL1611. GI:37988274  AKIL1611.1 GI:37988274  KEYWORDS  OTYZA SALIVA (japonica cultivar-group)  ORGANISM OTYZA SALIVA (japonica cultivar-group)  ORGANISM OTYZA SALIVA (japonica cultivar-group)  ORGANISM OTYZA SALIVA (japonica cultivar-group)  ELEATYOCA: VIXIdiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  ELATACTORIAN OTYZA SALIVA (japonica cultivar-group)  REFERENCE  ELATYORIAN OTYZA SALIVA (japonica cultivar-group)  REFERENCE  ANTHORS ARACOLII-Length cDNA CONSORTIUM, National Institute of Agrobio-daycal Sciences Rice Full-Length cDNA Project Team:, Kiknchi S. Sarch, K. Nagata, T. Kawaqashira, N. Doi, K.,	Kishimoto, N., Yazaki, J., Ishikwa, M., Yamada H., Ooka H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahaqi, W., Suzuki, K., Li, C., Ohteda, E., Yahaqi, W., Suzuki, K., Li, C., Ohteda, E., Yahaqi, W., Suzuki, K., Mikuza, Grome, Otomo, Y., Muzakani, K., Ida, Y., Sugune, Squencing & Analysis Group. Otomo, Y., Muzakani, K., Ida, Y., Suguyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikaroa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Mikura, J., Karoana, R., Mikura, J., Karusumagi, T., Oka, M., Raya, A., Mizuno, K., Yokomizo, S., Mikura, J., Kasumaj, T., Oka, M., Ryu, R., Mazuno, K., Yokomizo, S., Mikura, J., Kasumaj, T., Oka, M., Ryu, R., Mazuno, K., Yokomizo, S., Mikura, J., Kando, S., Kandi, J., Kaman, M., Hashidume, W., Hashidume, W., Hashidume, W., Hashidume, W., Hashidume, W., Hashidume, W., Hashidume, W., Hashidume, W., Shibata, K., Shinagawa, R., Shiraki, T., Yohino, M. and Hayashizaki, Y. Indoani, K., Shinagawa, A., Shiraki, T., Yohino, M. and Hayashizaki, Y., Hayashizu, M., Haranco, K., Hiranoco, M., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Kishima, Y., Kolno, H., Kobayashi, M., Kanagawa, S., Kathihawa, H., Kanama, Y., Kishikawa, H., Kishima, Y., Kolno, H., Koya, S., Kutihara, C., Kurosaki, T., Kishimoto, M., Kobayashi, M., Koya, S., Kutihara, C., Kurosaki, T., Kishima, Y., Kolma, Y., Mikura, J., Mikura, J., Mikura, J., Mikura, J., Mikura, J., Mikura, J., Mikura, J., Mikura, M., Satoh, M., Satoh, M., Sakai, K., Shinagawa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., Shinagwa, R., S	Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys
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Matches:
Conservative:
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  thaliana"
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  organism="Arabidopsis
                     /mol type="mRNA"
/variety="Columbia"
/db_xref="taxon:3702"
1. .1158
                                                                                                                                                      1. .1158
/gene="dpb"
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Submitted (06-SEP-2000) Magyar Z., Department Plantgenetica,
Laboratorium voor Genetica, Universiteit Gent, K.L. Ledeganckstraat
35., B-9000, Gent, BELGIUM
Location/Qualifiers
1. 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AJ294532
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Porlike protein; dpb gene.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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FEATURES

REFERENCE AUTHORS TITLE JOURNAL

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Bhalerao, R.P. and Sandberg, G.
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This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent this set was done by comparison with known proteins: two percent the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the crocked protein. Please note that these cDNA sequences are derived from the Ws or Laber ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequences from Col-0. Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
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pssrseqtitivutsasdttfqrlanldiqgddagsqgasgvkkkkrqqraagedktgr
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alnvlamni iskdkkeiqwrqlprislsdieelknerlslrnriekktaysqeleeg
yvglqnliqnrehlyssgnabsqqvalppliuvqtreplatveveisedbwqlydfnst
pfellhonfulktmkrcdqppqqnnsqlvchnftprnprqcyrgisedpyfpnyt
thlqsqqhqqusqlipmpysabdtavyssadtapvkspslprnyr
                                                                                                                                              AY086018 118 bp mRNA linear PLN 14-APR-2003
Arabidopsis thaliana clone 206791 mRNA, complete sequence.
                                                                                                                                                                                                                                                                                           Eukaryofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1618)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldmann, K.
Full-Length cDNA from Arabidopsis thaliana
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldmann, K.
                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1618)
Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N. Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome
                         AsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
                                                 1. .1618
/organism="Arabidopsis thaliana"
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db_xref="GI:21554147"
                                                                                                                                                                                                                                  FLI CDNA.
Arabidopsis thaliana (thale cress)
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/db_xref="taxon:3702"
/clone="206791"
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Alignment Scores:

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1640 bp mRNA linear PLN 31-DEC-2003 Populus tremula x Populus tremuloides transcription factor DP1 (DP1) mRNA, complete cds.
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Populus tremula x Populus tremuloides
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
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                                                                                                                                                                                                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGln 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 GlulleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGlu 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 IleArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLys 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluLysLysGluileArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLys 151
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768 GATADADADADATTCADTGGAGGTCTTCCTCGGACAAGCTTAAGCGACATTGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 ArglysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1008 ccrcacecaacagracaagracagararcagaagarargcagcrcgrecarrrrgarrrc
                                                                                                                                                                                                                                                                                                                                    37 GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys
                                                                                                                                                                                                                                                              97 LeuLysSerMetAlaHisIleGly------GlnGlyPheAspGluLysAsn
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1618
104
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68
6
                                    Conservative:
Mismatches:
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Unpublished
                                                                           Indels:
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Bhalerao, R.P. and Sandberg, G.
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Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Bukaryota; Viridiplantae; Stremuloides
Bukaryota; Viridiplantae; Stemuloides
Bukaryota; Wagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
I (bases I to 1640)
S Espinoza-Ruiz, A., Saxena, S., Schmidt, J., Mellerowicz, E., Bako, L. S.
and Bhalerao, R.P.
Differential stage specific regulation of cyclin dependent kinases during cambal dormancy in hybrid aspen
L Unpublished
L Unpublished
L Spinosa-Ruiz, A. and Bhalerao, R.P.
Direct Submission
L Submitted (27-MAY-2003) Department of Forest Genetics and Plant
Physiology, Swedish University of Agricultural Sciences (SLU), Umea
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963 CACTITGAITITAATAGCACTCCCTTCGAGCTCCATGACGATAATTACGTTCTCAAGGCA 1022
                                                                                                                                                                                                                                                                                                                                                                                     linear PLN 24-JUN-2003 (DP1) mRNA, complete cds.
                                                                                                                             227 HisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGly 246
                                                                                                      207 VallysThrSerArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAla 226
                                                  188 GlnThrieuGluSerSerAlaGluAsnValAsn---GlylleArgLeuProPheValLeu
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476.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspGluLysAsnIleArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArg 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 rerecarcageagegageargecargecacaceaeceaecraerageaecaceaecraera 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 AGGTTGAACCATCTCGACATTCACGCCGATGATGCCGCCACT------CAAGAT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 IleTyrSerGluLeuLysSerMetAlaHisIle-------GlyGlnGlyPhe 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::: :::||||
CTTGTCGCAGAGTTTGCTGACCCCAAGCAATAGTGTTTTCCACCCCAGATCAGCAATAT 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 ValileAlaLysGluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArgTyrGlu 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 LysileLysLysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLys 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GlyValHisIleLeuGluAlaSerSerValProProLeuProGlu 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 LysLysGluLysAlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLys 72
Submitted (31-AUG-1999) Department of Forest Genetics and Plant Physiology, SLU, Umea S-901 83, Sweden Location/Qualifiers
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                                                            1. .1640
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476.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 GITIGCAGACCCCAACAAIAATITIGCAICACCIGAICCIGACAACCCIAACACCACAC 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AlaproProArgGlyGlyAlaAlaAlaAlaAlaThrAlaAlaLeuAspLeuThrGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 HislleLeuGluAlaSerSerValProProLeuProGluAlaGlyGlyAsnAlaValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 ArglysGlyAlaVal-AspProAspLysAspArgLysLysGluLysAlaAlaAlaProAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 glleThr ------GlyTrpGlyLeuArgGluTyrSerLysIleValCysGl
                                                                                                                                                                                                                                                                                                                                                                                             'note="derived from yeast two-hybrid experiments"
                                                                                                              Guimil, S., Luginbuhl, P.,
                                                                                                                                                                                                                                                                                        (japonica cultivar-group)
                                                                                                           Cooper, B., Hutchison, D., Park, S., Guimil, S., Luginbuhl, P. Ellero, C., Goff, S. and Glazebrook, J.
Ellero, C., Goff, S. and Glazebrook, J.
Briect Submission
Submitted (17-13N-2003) Torrey Mesa Research Institute, S
Research and Technology, 3115 Merryfield Row, San Diego,
cyclin-mediated regulation of the cell cycle
Plant Mol. Biol. 53 (3), 273-279 (2003)
23111120
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                                                                                                                                                                                                                                           Location/Qualifiers
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57.61%
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Best Local Similarity:
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TF mRNA,
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
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                                                                                                                                                                                                                                                                                             ValileAlaLysGluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArgTyrGlu 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             722
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                                               291 rerecarceageageageargecargecacheceaecechecageageachtrerra 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                          93 IleTyrSerGluLeuLysSerMetAlaHisIle-------GlyGlnGlyPhe 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspGluLysAsnIleArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArg 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 LysileLysLysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLys 167
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                                                                                            --- GlyValHisIleLeuGluAlaSerSerValProProLeuProGlu 34
                                                                                                                                                                                                                                                                                                                                                                             903 GTGCAGACACGCCCTCATGCAACTGTTGAAGTGGAGATATCAGAAGATATGCAGCTGGTT
                                                                                                                                                                                 35 AlaGlyGlyAsnAlaValGlnArgLysGly-----AlaValAspProAspLysAspArg
                                                                                                                                                                                                                                                                    LysLysGluLysAlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLys
                                                                                                                                                                                                                                                                                                                                                     73 IlevalCysGluLysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGlu
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      AlaProProArgGlyGlyAlaAlaAlaAlaAlaThrAlaAlaLeuAspLeuThr-----
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Cooper, B., Hutchison, D., Park, S., Guimil, S., Luginbuhl, P.,
Ellero, C., Goff, S.A. and Glazebrook, J.
Identification of rice (Oryza sativa) proteins linked to the
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                                                                                                                         AY224551.1 GI:29367653
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317

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LOCUS DEFINITION

AY224551

SOURCE ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS

TITLE

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uArgValileAlaLysGluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArgTy 146

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AY224589
Oryza sativa (japonica cultivar-group) isolate 31182 E2F
dimerization factor mRNA, complete cds.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatrophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1140)
Cooper, B., Hutchison, D., Park, S., Guimil, S., Luginbuhl, P.,
Ellero, C., Goff, S. A. and Glazebrook, J.
Identification of rice (Oryza sativa) proteins linked to the
cyclin-mediated regulation of the cell cycle
Plant Mol. Biol. 53 (3), 273-279 (2003)
                                       TTTGCACTTCCAAATAACGATGGAACATCCCCTGATCAGCAACAGTATGATGAGAAAAAC 459
                                                                               131
                                                                                                                                                                                                                                                      192 SerSerAlaGluAsnValAsn---GlyIleArgLeuProPheValLeuValLysThrSer 210
                                                                                                                                                                                                                                                                                                                                                                                                            211 ArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPhe 230
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                                                                                                                                                                                                                                LeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGln 171
                                                                                                                                                                                                                                                                                                            GlulleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGlu 191
                                                                                                                                                       132 GlulyslysglulleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLyslleLysLys 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1140)
Cooper, B., Hutchison, D., Park, S., Guimil, S., Luginbuhl, P.,
Ellero, C., Goff, S. and Glazebrook, J.
Direct Submission
Submitted (27-JAN-2003) Torrey Mesa Research Institute, Syngenta
Research and Technology, 3115 Merryfield Row, San Diego, CA 92121,
USA
                                                                         ------AGAAATGAGCACTTATAT
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                                                                                                                                                                                                             669 GGCACAGGGAAACGAGCTTTATGGTTCAGGAAATGCTCCTTCAGGAGGAGTGGCATT 728
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729 GCCATTTATATTGGTGCAGACACGTCCTCATGCTACAGAAGTGGAGATATCAGAAGA 788
                                                                                                                                                                                                                                                                                                                                                                  Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
Nucleic acid molecules encoding plant cell cycle proteins and uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AlaAlaAlaProArglleThrGlyTrpGlyLeuArgGluTyrSerLyslleValCysGlu 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 LysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGlu 96
                                                                                                                                   -----AsnLysil
                                                         eArgAsnLysLysAlaLeuLeuGlnGluIleGluLysGlnPheAspAspLeuGlnAsnIl
                                                                                                                                                                                       eLysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlyIleArgLe
                                                                                                                                                                                                                                                                  uProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIleSerAspAs
                                                                                                                                                                                                                                                                                                                                            pSerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSe
498. GGATATTATATCTAAGGATAAAAGGAAATTCAGTGGAAGGGCTTGCCTCGG-------
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Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheol
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots,
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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CropDesign N.V. (BE)
Location/Qualifiers
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Sequence 33 from Patent W00185946.
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AX449314
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ACTGTGGAAGTTGAAATATCAGAAGATATGCAACTTGTACATTTTGACTTTAATAGCACA

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ASTSGGSAGSPSSRSEQHVPAAAGMAAGAAASTPISENTFILRINDLDIHGDDAPSSQ APTSKKKKRGARAKOGPDKGGRGLRQFSAMKVCEKVESKGRTTYNBVADELVABFADPNN SILPPDPDNPNAQQYDEKNIRRVYDALANVLMAMEIISKOKKEIQWKGLPRTSINDIE DLQTELVGLKSRIEKRYTLQBLQDQFVGMQKLIQRNEQLYGSGNIPSGGVALPFILV QTRPHATVEVEISEMOLVHPDFNSTPFELHDDSFVLKAMSSCGEEQIDGIHDLISNG GESSSMPNIYRQQVQQPARSTNGTARLPSSPPIPGILKGRVKHEH" translation="MVSGVAHRPDDDGGRAASTFQRPPQPAGARPSLATPPPSGGAQS" 147 22 ---LeuProGluAla 1140 111 43 77 63 Length:
Matches:
Conservative:
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138 618 699 213 ArgValGluIleGluIleSerAspAspSerLysPheAlaHiePheGluPheAsnGlyAla 233 438 MetGlyLeuSerAsnTyrArgTyrGluLysIleLysLysLeuGluGluValArgLysGlu 158 Leuval -----AsnLysIleArgAsnLysLysAlaLeuLeuGlnGluIleGluLys 175 GlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSerAlaGlu 195 198 258 318 378 103 499 CCGGATAATCCCAATGCACAACAATATGACGAGAAAAATATACGGAGAGAGGGTTTATGAT 558 88 48 48 68 GluTyrSerLys1leValCysGluLysValGluAlaLysGlyArgThrThrTyrAsnGlu AsnVal-----AsnGly1leArgLeuProPheValLeuValLysThrSerArgLysAla ProProArgGlyGlyAlaAlaAlaAlaAlaThrAlaAlaLeuAspLeuThrGlyValHis 199 GCAGGCATGCCGGGGGGGGGGGGGCGCCCTTACTCCGATTAGTGAGAATACCTTCCTC 259 CGCCTCAACGACCTTGACATCCACGGCGACGATGCGCCTTCCTCACAGGCTCCAACGAGC AlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLysLysGluIleArgTrp AsplysAspArglysLysGluLysAlaAlaAlaProArgIleThrGlyTrpGlyLeuArg ValAlaAspGluIleTyrSerGluLeuLysSerMetAlaHisIle------109 CCGCCCTCGGGCGGAGCGCAATCCGCTTCGACGAGCGGC-----36 GlyGlyAsnAlaValGlnArgLysGlyAlaValAspPro-23 IleLeuGluAlaSerSerValProPro----US-10-088-830-2 (1-261) 49 319 69 379 439 559 139 730 196 787 М 148 48 89 104 119 159 670 176

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	PAT 03-JUL-2002 ta, Tracheophyta;	eae; Arabloopsis. J.A. and Magyar,Z. cycle proceins and uses		rglyslysGlulys 56 ::::: AGAGGGACAGCGT 379	GAAAGGTCTTATC 439	-IleValCysGluLysValGlu 79 :::            TTCAATTGTGAAAGGTGGAA 499	rGluLeuLysSer 99 :     :TGAATTTGCACTT 559	rsAsnIleArgArg 114 	.aLysGluLysLys 134 ::   :::       :CAAGGATAAAAA 679
lyVal 247 ::: CAATG 948	op)	c]e.,	1442 103 : 41 68 34	Splysaspar     	luTyrSerly :::::    AATTTAGTA	IlevalCy :::  TTTCAATTT	lulleTyrSe   :::  AGCTTGTTG	-GlnGlyPheAspGluLysAsnIl      :::           GCAACAGTATGATGAGAAAAACAT	rgValileA :::   : ATATAATAT
ProPheThrLeuHisAspAspLeuSerIleLeuGluGlyVal 	2 bp 185946. cress) treptop a; eudi	'assicales, Brassi. ' Veylder, L., Acos encoding plant ce . 15-NOV-2001; . fiers bidopsis thaliana issigned DNA"	Length: Matches: Conservative Mismatches: Indels: Gaps:	GlyabnalaValGlnargLysGlyalaValaspProAspLysAspArgLysLysGluLys     ::: 	alaalaalaproargilethrglytrpglyLeuargglutyrSerLys		AlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer :::	TGATCA	ArgValTyrAspAlaPheAenValLeuileAlaLeuArgValileAlaLyeGluLyeLye 
LeuHisaspaspLei              TGCATGATGACTC	from Patent WO0 GI:21698089 thaliana (thale thaliana Viridiplana viridiplana	rosids; eurosids II; Brasslcales Inze,D., Boudolf,V., de Veylder, Nucleic acid molecules encoding therefor Pacent: WO 0185946-A 61 15-NOV-2 CropDesign N.V. (BB) Location/Qualifiers 11442 /organism="Arabidopsis/mol_type="unassigned D/mol_type="unassigned 31e-28 456.00 41.874 34.574 5	ValGlnArgLysGl  -::    GCTGGTTCTCAAGG	ProArglleThrGl       CCAGATAAGACTGG	GCCCCTATTATGCT	AlalysglyargThrThrTyrAs :::              agcaaggaaggacaacttacaa	SIleGly     GATGGAACATCCCC	cAspAlaPheAsnVa            GATGCTTTAAACGT	
234 ProPheThrLeuHi         907 CCATTTGAGTTGCA	AX449342 Sequence 61 AX449342 AX449342.1 Arabidopsis Arabidopsis Bukaryota; Spermatophy	rosids; eurc linze,D., Bol Nucleic acid therefor Patent: WO ( CropDesign I 10, (m)	<pre>ment Scores:    No.:    s:    tit Similarity:    Local Similarity:    Match:     Match:    O88-830-2 (1-261)</pre>	r 0	57 AlaAlaAle        80 GCGGCTGG1	73	80 AlaLysGly :::       500 AGCAAAGG	0 0	115 ArgValTy          620 AGAGTATAT
Qy 23	AX449342 AX449342 DCCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	Alignment Sco- Pred. No.: Score: Percent Simil. Best Local Si Query Match: DB: US-10-088-830	Qy 32	50 40 136	. Ad	Oy GO	Oy 10 Db 56	ζγ 1: Db 6:

Ecker, J.R. (SSP/Salk)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 ATTAAGCAAAACGCAGAGAAGCCTTTGAATGAAAATGAGTACAATGAGAAGAACATAAGG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 ArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLys 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 GluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGlnGluIle 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 GlulysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSer 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGlnArgiyşGlyAlaValAspProAspLysAspArgLysLysGluLysAlaAlaAla 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 CGGAGAGTCTACGATGCGCTCAATGTGTTCATGGCGTTGGATAATATTATTGCAAGGGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 ACTCAAGGCCCAGCAGAAGGATTACCTTACCATTCATTCTACTAGACAAACCCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 ATGGATCGTAATAAAGTTATGAGCAGTGTGCAAAAGAAGGCTGCTTTTCTTAAAGAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                    'note="putative DP-2 transcription factor"
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Conservative:
Mismatches:
Indels:
                       contributed equally to this work as PIs
Location/Qualifiers
                                                                                                                                                                                                                                                                                                     /ecotype="Columbia"
/note≂"This clone is in pUNI
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                                                                                                             l. .8/>/
/organism="Arabidopsis
      (RIKEN
                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:3702"
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                                                                FEATURES
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Kim.C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kanla, A., Karlin. Heumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Ondera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Sakou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
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Kim.C.J. Chen.H., Cheuk.R., Shinn,P., Bowser,L., Carninci,P.,
Chan,M.M., Chang,C.H., Dale,J.M., Hayashizaki,Y., Hsuan,V.W.,
Ishida,J., Jones,T., Kannya,A., Karlin-Neumann,G., Kawai,J.,
Iam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Sarcu,M., Seki,M.,
Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K.,
Yu,G., Yuan,S., Shinozaki,K., Davis,R.W., Theologis,A. and
Beker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    980 ATGCAGCTCGTGCATTTTGATTTCAACACCTCCATTTGAGCTCCACGACGACAATTTT 1039
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                            ProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIleSerAspAsp 222
                                                                                                                                                                                                                                                                                                                                                                                      SerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSer 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim,C.J., Chen,H., Cheuk,R., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collection and clustering of RAFL cDNAS (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                       184 LysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlylleArgLeu
                                                                                                                                                                   ----LeuGlnAsnIle
                                                         GAACAÁGTAATGAACATCGATACTCTCGGCTTATCTGCTTCCTGCCTTCAGAATCTG
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AlaArgValGlu1leGlu1leSerAspAspSerLy8PheAlaHisPheGluPheAsnGly 232

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to

COMMENT

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 14 ATH319027

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AUTHORS TITLE JOURNAL REFERENCE

REFERENCE

TITLE JOURNAL

EATURES

AUTHORS

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                 154 GluValArgiysGluLeuValAsnIysIleArgAsniysiysAlaLeuLeuGlnGluIle 173
                                                                                                                                                                                                                                                                                                                                                                                                                   174 GluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSer 193
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                                                                                                                                                                                                                                                                        LysGluileArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLysLeuGlu 153
                                                                                                                                                         :::
337 ATTAAGCAAAACGCAGAGAAGCCTTTGAATGAAAATGAGTACAATGAGAAGAACATAAGG
                                                                                                                                                                                                                                                                                                          457 AAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGAAGTCAAG
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577 AGAGAAAAGGTCTCAAGAGTCTTAAGTCTTATGTCGAGAAATCAAGAGATGGTTGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 AlaGluAsn---ValAsnGlyIleArgLeuProPheValLeuValLysThrSerArgLys
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Nucleic acid molecules encoding plant cell cycle proteins and
therefor
                                                        AlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer
                                                                                                                               MetalaHisIleGlyGln------GlyPheAspGluLysAsnIleArg
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AX449297
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AFLKELRENTPPSYHDDAYILKLMQEQKQEQNRVSSSSSTHHQSQHSSAHSSSSSCIAS

GYRGPPSYVNNSSSIDTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (29-AUG-2001) Bergounioux C., UMR 8618, Chrs, IBP bat 630
Universite Paris-Sud, 91405 Orsay, FRANCE
Location/Qualifiers
                                                                                                                                                      ATH319027 960 bp mRNA linear PLN 29-JAN-2002
Arabidopsis thaliana partial mRNA for E2F dimerisation partner
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         GCAGTAGTCGAAATCGAGATTTCTGAAGATATGCAACTTGTACACCTCGACTTCAATAGC 678
                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                               E2F family transcription factors: AtE2F-a and AtDP-a, induce Arabidopsis leaf cells to re-enter S phase Unpublished 2 (bases 1 to 960)
Bergounioux,C.
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dpza gene; BzF dimerisation partner protein.
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154 GluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGlnGluIle 173
                                      100 MethlaHisIleGlyGln--------GlyPheAspGluLysAsnIleArg 113
                                                                                                                                                                                                     134 LysglulleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLysLeuGlu 153
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512 AGAGAAAAGGTCTCAAGTCTTGAGAGTCTTATGTCGAGAAATCAAGAGGTTGTGAAG 571
                                                                                                                                                                                                                                                                                                                                                                     213 AlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPheAsnGly 232
                                                                                                                                                                                                                                                                                                                                                                                 212 GCCAAGAAGATAACTACTTACAAGGAGGTTGCAGACGAAATTATTTTCAGATTTTGCCACA 271
                                                                                                                                  194 AlaGluAsn---ValAsnGlyIleArgLeuProPheValLeuValLysThrSerArgLys 212
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40 ValGinargiyeGiyalaValaspProAspiyeAspArgiysiysiysGiuiysAlaAla 59
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E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MODEL-frame+ prin, model - DEV=xlh - Q4022005_122602_29549/app_query.fasta_1.455 - G2-(cgn2_1/USPTO_spool/US10088830/runat_04022005_122602_29549/app_query.fasta_1.455 - DEA_GGn2_1/USPTO_spool/US10088830/runat_040271.xrg - MINMATCH=0.1 - LCOPCE.0 - L-LCOPCE.0 - L-LCOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15 - MODE=LOCAL - OUTFMT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=200000000 - USRR=US10088830_@CGN_1 1 + 470_@TUNAT - DSPENOCK=100 - LONGE - ICPU=3 - NO MMAP - LARGEQUERY - NGG SCORES=0 - WAIT - DSPENOCK=100 - LONGLOG - LONGLOG - DSV_T INBOUT=120 - WARN_TINBOUT=30 - THREADS=1 - XGAPOP=10 - XGAPORT=0.5 - FGAPOP=6 - DELOP=6 - DELOP=6 - DELOP=6 - DELOREXT=7
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Ado63082 Transcrip
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                                                                                                                                  February 6, 2005, 18:50:47; Search time 583 Seconds (without alignments) 2650.176 Million cell updates/sec
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                                                                                                                                                                                                                                                                  MAPPRGGAAAATAALDLTG......SILEGVRRNSIGRAGRATLH
                   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                 using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AAC39795
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                                                                                                                                                                                                                                                                                            BLOSUM62
Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Fgapop 6.0 , Fgapext 7
Palop 6.0 , Delext
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geneseqn2001bs:*
geneseqn2002as:*
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Maximum DB seq length: 200000000
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Match Length
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Aah33503 Human col Aag65344 Transcrip Adr65325 Cotton cD Ado63216 Transcrip Aas94979 Human DNA Ado62851 Transcrip

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The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related nucleic acid sequence. The present sequence is published separately from the main body of the specification as EPO data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell proliferation related polypeptide; cell proliferation; senescence; differentiation; stress response; ds.
                    GlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsnGlyIle
                                                                                                      620 ceccriccariceraticarcaacarcraceaaaccaaccaaccaaccaaarracaaarraca
                                                                                                                                           AspAspSerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAsp
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                                                                                                                                                                                                                                     740 CTCTCAATCCTTGAGGGGGTAAGGCGTAACAGCATAGGAAGAGAGCTGGCCGCGCCCCCTT
                                                                                                                                                               New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U; 0 Other;
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Best Local Similarity:
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                                                                                                                                                                                                                            The present sequence encodes a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue so to alter plant cell, organ or tissue
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                                                                                                                            New isolated, enriched, cell free and/or recombinant nucleic acid use for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.
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                                      Ramirez-Parra E;
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Plant; transcription factor; transgenic plant; abiotic stress tolerance; sencits stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                             Reuber TL;
                                                                                                                                             Adam LJ, R
Sherman BK;
Transcription factor G2981 coding sequence, SEQ ID 1549
                                                                                                                                            Creelman RA,
, Keddie JS,
                                                                                                                                            Ratcliffe O, C
V, Dubell AN,
                                                                                                                               (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                          17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                                       18-SEP-2003; 2003WO-US030292
                                                                                                    18-SEP-2002; 2002US-0411837P
                                                                                                                                            Jiang C, Heard JE,
Riechmann JL, Haake
                                              Arabidopsis thaliana
                                                            WO2004031349-A2
                                                                         15-APR-2004
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New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.

WPI; 2004-330163/30. P-PSDB; ADO63083.

Claim 1; SEQ ID NO 1549; 510pp; English.

tungal disease and particularly Expsiphe, Fusarium and Botrytis, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ACC, altered sensing, increased tolerance to sugars, altered flower structure, loss of flowering, latered flower structure, loss of flowering, altered shoot meristem development, altered branching pattern, altered stem morphology, altered velopment, altered branching pattern, altered trichome structure, altered sensitivity, altered sed sed apical dominance, altered trichome density, altered trichome development, altered sed call proliferation, altered sed development, altered sed sed call proliferation, altered sed sed development, altered sed dipase change, altered sensecence, abnormal embryo development, altered programmed cell called sensescence, abnormal embryo development, altered plants, increased cell prices, altered branching, altered plants, death, lethality when overexpressed, altered necrosis patterns, increased call are, increased blomass, large seedlings, dwarfed plants, green leaves, change in leaf shape, increased leaf size and mass, light green cr gray leaves, altered seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed sed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large seed shape, large see decréased anthocyanin levels. Note: The sequence data for this patent did The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold, increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed brotein content, altered seedprenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and form part of the printed specification, but was obtained in from WIPO at

Sequence 1158 BP; 374 A; 261 C; 253 G; 270 T; 0 U; 0 Other;

ftp.wipo.int/pub/published\_pct\_sequences

ADO63082 standard; DNA; 1158

(first entry)

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Plant; transcription factor; transgenic plant; abiotic stress tolerance; cosmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                    Transcription factor G2981 coding sequence, SEQ ID 609
                                                                                                                                                                                        Arabidopsis thaliana
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The present invention relates to novel plant transcription factor proteins (I) and nuclectide sequences (II) (ADO6154-ADO6179). The equences can be used to produce transgenic plants which overexpress (II), where the transgenic plant has an altered trait as compared to a control of the transgenic plant comprises on non-transgenic plant of the transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to conditions, increased tolerance to disease, increased tolerance to mitrogen conditions, increased tolerance to disease, increased tolerance to multiple fungal pathogens, increased tolerance to multiple fungal pathogens, increased tolerance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABC, altered sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced density, altered to ABA, altered sensitivity to ABA, reduced density, altered send trichome structure, altered sensitivity to ABA, altered send fored plants, altered send fored plants, altered sensitivity to ABA, altered sensitivity to ABA, altered sensitivity to ABA, altered sensitivity to ABA, altered sensitivity sensitivity and 
                                                                                                                                                                                                                                                                                                                                                 New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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Keddie JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 609; 510pp; English.
                                                                                                                                                                                                                  liffe O, C. Dubell AN,
                                                                                                                                                                        (MEND-) MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                    Jiang C, Heard JE, Ratcliffe
Riechmann JL, Haake V, Dubell
                                                                                                                               24-APR-2003; 2003US-0465809P.
                                         18-SEP-2003; 2003WO-US030292.
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17-DEC-2002; 2002US-0434166P.
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Matches: Conservative: Mismatches: Indels: Gaps: 1.24e-39 492.00 66.06% 47.71% 37.30% Similarity: Percent Similarity: Best Local Similari Query Match:

1158 104 40 68 6

Length:

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GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys 56 37

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 TTTGCACTTCCAAATAACGATGGAACATCCCCTGATCAGCAACAGTATGAGAAAAAC 459
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                                                                                                                                                                                                    LeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGln 171
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                                                                                                                                IleArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLys
                                                          LysValGluhlaLysGlyArgThrThrTyrAsnGluValAlaAspGlulleTyrSerGlu
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                         AlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGlu
                                                                                                                                                                                                                                                                                                                                              AsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana DNA fragment SEQ ID NO: 25934
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99US-0123180P.
99US-0125548P.
99US-0126264P.
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99US-0127462P.
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09-MAR-1999;
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01-APR-1999;
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9US - 0.1443339 9US - 0.14433189 9US - 0.1443259 9US - 0.1446329 9US - 0.14468149 9US - 0.14508679 9US - 0.14508679 9US - 0.14508979 9US - 0.14508979 9US - 0.14518979 9US - 0.14518979 9US - 0.14518979 9US - 0.14518979 9US - 0.14518979	990S-01453919P 990S-0146386P 990S-0146388P 990S-0147038P 990S-0147204P 990S-0147102P 990S-0147102P 990S-0147102P 990S-0147103P 990S-0147103P 990S-0147103P 990S-0147103P 990S-0147103P 990S-0147103P 990S-0147103P 990S-0147103P 990S-014938P 990S-014938P 990S-014938P 990S-014938P 990S-014938P 990S-014938P 990S-014938P 990S-014930P 990S-014930P 990S-014930P 990S-014930P 990S-014930P	905 - 0151000 905 - 0151000 905 - 0151000 905 - 0151000 905 - 01530700 905 - 01530700 905 - 01551390 905 - 01551390
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172 GlulleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGlu 191

587

92

56 527

37 GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys

US-10-088-830-2 (1-261) x AAC39795 (1-1618)

468 GGTGATGATGCTGGTTCTCAAGGAGCTTCTGGTGTTAAGAAGAAGAAGAGGGGACAGCGT

8 8 8

111

648 TTTGCACTTCCAAATAACGATGGAACATCCCCTGATCAGCAACAACATGAGAAAAAC 707

97 LeuLysSerMetAlaHisIleGly------GlnGlyPheAspGluLysAsn

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	Length: Matches: Conservative: Mismatches: Indels: Gaps:
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## ## ## ## ## ## ## ## ## ## ## ## ##	Aligr Pred Score Perce Best Query DB:

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The present invention relates to novel plant transcription factor

proteins (I) and nucleotide sequences (II) (AD061534-AD063778). The

sequences can be used to produce transgenic plants, which overexpress

(II), where the transgenic plant has an altered trait as compared to a

contransgenic plant or wild-type plant. The transgenic plant comprises

constraints selected from increased tolerance to abiotic stress,
increased germination in cold, increased tolerance to heat, increased

concreased germination in cold, increased tolerance to heat, increased

concreased germination in cold, increased tolerance to heat, increased

concreased tolerance to low nitrogen conditions, increased tolerance to

concreased tolerance to low nitrogen conditions, increased tolerance to

concreased tolerance to multiple fungal pathogens, increased tolerance to

concreased tolerance to multiple fungal pathogens, increased tolerance

concreased sensitivity to ABC, altered sugar sensing, increased tolerance

concreased sensitivity to ABC, altered sugar sensing, increased tolerance

concreased sensitivity to ABC, altered sugar sensing, increased tolerance

concreased sensitivity to ABC, altered sugar sensing, increased tolerance

concreased sensitivity to ABC, altered sugar sensing, increased tolerance

concreased sensitivity to ABC, altered sugar sensing, increased tolerance

concreased sensitivity to ABC, altered sensing, early flower determinacy, reduced

fertility, altered shoot meristem development, altered branching pattern,

concreased stem morphology, altered vascular tissue structure, altered seed development, altered seed development, altered seed development, altered call definentiation,

altered trichome structure, altered vascular tissue structure, altered seed development, altered cell definentiation,

altered call proliferation, altered cell expansion, altered seed of development, altered seed development, altered seed development, altered seed cell expansion, altered senses cence altered senses cence altered sense cence 
                      CTCACGCAACAGTAGAAGTGGAGATATCAGAAGATATGCAGCTCGTGCATTTTGATTTC 1067
                                                                                                                                                                                                                                                                                                                                                                                                                              Plant; transcription factor; transgenic plant; abiotic stress tolerance; semcitic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low hosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
211 ArglysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPhe
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                                                                                                                       AsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
                                                                                                                                                                                                                                                                                                                                                                                    Transcription factor G2981/2982 orthologous sequence, SEQ ID 1319.
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Sherman BK;
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17-DEC-2002; 2002US-0434166P.
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Riechmann JL,
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death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased biomass, large seedlings, dwarfed plants, dark green leaves, charge in leaf shape, increased leaf size and mass, light spreen or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed protein content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 ArgValileAlaLysGluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArgTyr 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               636 ACAGCCIATCTGCAGGAGCTTGAGGAGCAATTCGTAGGTCTTCAGAACCTTATTCAACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            756 TTGGTACAGACACGTCCTCATGCAACTGTGGAAGTGGAAATATCAGAAGATATGCAGCTT
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                                                                                                                                                                                                                                              Other;
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Matches:
Conservative:
Mismatches:
Indels:
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altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seedprenyl content, altered seedprenyl content, altered seedprenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels, and the content seed seed for this patent of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel plant transcription factor proteins (1) and nucleotide sequences (11) (AD061534-AD063778). The sequences can be used to produce transgenic plants, which overexpress (CI), where the transgenic plant has an altered train secondared to a non-transgenic plant or wild-type plant. The transgenic plant comprises or non-transgenic plant or wild-type plant. The transgenic plant comprises or non-transgenic plant or wild-type plant. The transgenic plant comprises or non-transgenic plant or wild-type plant. The transgenic plant comprises or non-transgenic plant or wild-type plant. The transgenic plant comprises or non-transgenic plant or wild-type plant. The transgenic plant compliance or off confidence or cold, increased tolerance to deceased tolerance to cold, increased deceased tolerance to decease deceased tolerance to low phosphate conditions, increased tolerance to maltiple fungal pathogens, increased tolerance to multiple fungal pathogens, increased tolerance to glyphosate, increased sensitivity to ACC, altered sugar sensing, increased resistance to glyphosate, altered carbon/nitrogen sensing, early flowering, late flower studied sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered darbon/nitrogen sensing, early flowering, latered flower studied wevelopment, altered branching pattern, altered altered trichome erroture, ratered vevelopment, altered development, altered development, altered coll dominance, altered trichome density, altered coll dominance, altered trichome density, altered coll dominance, altered trichome density, altered coll proliferation, altered coll development, altered seed development, altered seed coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered 
                                                                                                                                                                                                                                                                                                         Plant; transcription factor; transgenic plant; abiotic stress tolerance; somedic estress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to novel plant transcription factor
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Sherman BK;
                                                                                                                                                                                                                                                                   Transcription factor G2981/2982 orthologous sequence,
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V, Dubell A
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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         246 GlyValArg
                                    876 GCAATGAAA
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Riechmann JL,
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                                                                                                                                                                                                                                                                                                                                                                                75 CysGluLysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyr
                                                                                                                                                                                                                                                                                                                                                                                                 249 TGTGAGAAAGTGGAAAGCAAAGGAACTACGTATATATGAGGTTGCAGATGAACTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 GCTGAGTTTTCTGATGCTACCAATAGTGTTGCAGGCTCAGATCAGAACAATATGATGAG
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                                                                                                                                                                                                                    -------GlyValHisIleLeuGluAlaSerSerValProProLeuProGlu
                                                                                                                                                                                                                                                                                                                              55 GluLygAlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIleVal
                                                                                                                                                                                                                                    2 AlaProProArgGlyGlyAlaAlaAlaAlaAlaThrAlaAlaLeuAspLeuThr-
Sequence 1153 BP; 337 A; 225 C; 267 G; 324 T; 0 U; 0 Other;
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114
40
82
31
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                                       Length:
Matches:
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Mismatches:
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uArgValijeAlaLysGluLysLysGluIjeArgTrpMetGlyLeuSerAsnTyrArgTy 146
                                                                                             GTTTGCAGACCCCAACAATAATTTTGCATCACCTGATCCTGACAACACCAAACACACAA 437
                                                                                                                                                                                                                       107 -PheAspGluLysAsnIleArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLe 126
                                                                                                                                                                                                                                                                                                                                                                      146 rGluLyslleLysLysLysLeuGluGluValArgLysGluLeuVal------AsnLysll 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cycle protein, CCP, ss; cell cycle regulation, herbicide;
t growth regulator; plant development; abiotic stress; biotic stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 ATTTGATGAGAAAATATACGACGACGAGGTTTATGGTGCATTGAATGTCCTGATGGCTAT
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                                                                          76 uLysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGl
                                                                                                                                                                                                                                                                                                                  :::|||:::|||:::|||498 GGATATTCAGTGGAAGGCTTGCCTCGG-------
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     ----GlyTrpGlyLeuArgGluTyrSerLysIleValCysGl
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                                                                                                                                                96 uLeuLysSerMetAlaHisIleGlyGlnGly---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related nucleic acid sequence. The present sequence is published separately from the main body of the specification as EPO data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 HisileLeuGluAlaSerSerValProProLeuProGluAlaGlyGlyAsnAlaValGln 41
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                                                                                                                                                                                                                                                       cell proliferation related polypeptide; cell proliferation; senescence; differentiation; stress response; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecule encoding a cell proliferation-related bolypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and producing enhanced food crops.
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                                                                                                                                                                                                                     Cell proliferation-related nucleic acid sequence #2.
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ArgasnSerIleGlyArgAla 255
                                    ---AATTTTTGCGGAAGATCA 803
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41.30%
35.75%
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                                                                                                            standard;
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Best Local Similarity:
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Tue Feb

P-PSDB; AAU72514. 

New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.

Claim 38; Page 185-186; 316pp; English.

The invention relates to a novel cell cycle protein (CCP) and the polynucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the copyapptide and which binds to the polypeptide and which binds to the copyapptide and which binds to the copyapptide and which binds to the copyapptide and anti-CCP antibody is useful for medulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CC nucleic acid and polypeptide molecules are useful as modulating agents in cegniating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein or production of CCP protein forms which have decreased or observant activity. Compounds that bind to or modulate the activity of CCP polymucleotide are useful for modifying cell fate, plant development, of polymucleotide is useful for modifying cell fate, plant development, of plant morphology, blochemistry and/or physiology, the length of the CCP plant morphology, blochemistry and/or physiology, the length of the CCP companies or all plants, initiation, promoction, stimulation or enhancement of cell division, DNA replication, promoction, stimulation and/or development, nodule function, dwarfism in plants, compacted and activity of a protein involved in the cell cycle due to protein levels or activity of a protein involved in the cell cycle due to protein levels or activity of a protein involved in the cell cycle due to protein levels or activity of a protein involved in the cell cycle due to protein levels or activity of a protein involved in the cell cycle due to plant architecture, plant quality traits, plant reproduction and seed development, endereduage cells, serons enderedual or address protein in storage cells, and attenuate or address protein in storage cells, and immuned or and repress such as immuned or an immuned or an immuned or an storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally cocurring CCP substrates. The polynucleotide is useful for expressing CCP protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence encodes a CCP protein of the Invention

BP; 366 A; 256 C; 247 G; 262 T; 0 U; 0 Other; Sequence 1131

220 GGTGATGATGCTGGTTCTCAGGAGCTTCTGGTGTTAAGAAGAAGAAGAAGAGGGGACAGCGT 279 gcggcrggrcchgaraagacrggaagagagcracgrcaarrragrargaaagrrrgrgaa 339 -----GinGlyPheAspGluLysAsn 111 400 TTTGCACTTCCAAATAACGATĠĠAACATCCCCTGATCAGĊAACAGTATĠATĠAĠAAAAĊ 459 IleArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLys 131 57 AlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGlu 76 37 GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys 56 LysvalGluAlaLysGlyArgThrTyrAsnGluValAlaAspGluIleTyrSerGlu 96 Length: Matches: Conservative: Mismatches: [ndel8: LeuLysSerMetAlaHisIleGly-----Gaps: x AAS96304 (1-1131) .36e-37 466.50 63.76% 46.33% 35.37% US-10-088-830-2 (1-261) Similarity: Percent Similarity: Alignment Scores: 280 11 340 97 112 Query Match: Best Local g 셤 g 엄 ò ò ઠે ò ò

171 639 732 230 733 CCTCACGCAACAGTAGAAGTGGAGATATCAGAAGATATGCAGCTCGTGCATTTTGATTTC 792 GlulyslysgluileArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysileLysLys 151 GluileGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGlu 191 520 GATAAAAAAGGAATTCAATGGAGAGGTCTTCCTCGGACAAGCTTAAGCGACATTGAAGAA ------AGAAATGAGCACTTATAT SerSerAlaGluAsnValAsn---GlyIleArgLeuProPheValLeuValLysThrSer LeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGln 580 TTAAAGAACGAACTCTCACTTAGGAACAGAATTGAGAAGAAAACTGCATATTCCCAA 211 ArglysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPhe 248 AACAGCACTCCATTTGAGCTCCACGACGACAATTTTGTCCTCAAGACTATGAAG 846 231 AsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg GAACTGGAAGAACAA 640 192 793 172 152 g g Š 셤 ठे g ò g ò 셤 8

ADQ36854 standard; DNA; 1140 BP ADQ3685.

ADO36854;

(first entry) 07-OCT-2004

cell proliferation related polypeptide; cell proliferation; senescence; differentiation; stress response; ds. Cell proliferation-related nucleic acid sequence #7.

Oryza sativa.

WO2004061122-A2.

22-JUL-2004

23-DEC-2003; 2003WO-US041200.

26-DEC-2002; 2002US-0436565P.

(SYGN ) SYNGENTA PARTICIPATIONS AG.

Cooper B;

WPI; 2004-534388/51.

New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. 

Claim 3; SEQ ID NO 13; 408pp; English.

modulating cell proliferation, sensocence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related nucleic acid sequence. The present sequence is published separately from the main body of the specification as EPO data. encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for The present invention relates to an isolated nucleic acid molecule

Sequence 1140 BP; 327 A; 268 C; 310 G; 235 T; 0 U; 0 Other;

Alignment Scores:

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119 AAGAAGAAGAAGAGGACCACGAGTTGGTCCTGACAAAGGTGGCAGGGGGTTTTTTT
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439 GTGGCAGATGAACTTGTTGCGGATCCCAATAACAGCATTTTGCCACAGAT 498
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                                                                                                                                                                                                                                                                                           259 CGCCTCAACGACCTTGACATCCACGGCGACGATGCGCCTTCCTCACAGGCTCCAACGAGC 318
                                                                                                                                                                                                                                                                                                                                                                                                                     ValAlaAspGluIleTyrSerGluLeuLysSerMetAlaHisIle------ 103
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 1140
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63
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                              23 IleLeuGluAlaSerSerValProPro----
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  4.41e-37
             466.50
52.38%
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ADO63363 standard; DNA; 1245 BP

RESULT 11
ADO63363
ID ADO6

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Plant; transcription factor; transgenic plant; abiotic stress tolerance; sometic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                           New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                             Reuber TL;
                        Transcription factor G2981 orthologous sequence, SEQ ID 1830.
                                                                                                                                                             Adam LJ, Ro
Sherman BK;
                                                                                                                                                             Creelman RA,
Keddie JS,
                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1830; 510pp; English.
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                                                                                                                                                           d JE, Ratcliffe O,
Haake V, Dubell A
                                                                                                                                                (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                         18-SEP-2003; 2003WO-US030292
                                                                                                                       18-SEP-2002; 2002US-0411837P
                                                                                                                             17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
            (first entry)
                                                                                                                                                                                WPI; 2004-330163/30.
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                                                                                 WO2004031349-A2.
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Riechmann JL,
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WPI; 2000-524530/47.
P-PSDB; AAB07975.
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                                                                                                                                                                                                           ---IleGlyGlnGlyPheAspGluLysAsnIle 112
                                                                                                                                                                                                                                                                                247 AATATTGAGGCACCAGATCCTGATAACCCTAACGCGCAACAATATGATGAGAAAAATATA 306
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Mismatches:
Indels:
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The present sequence encodes a corn DP (not defined) polypeptide. The polypeptide is a transcription factor that activates transcription of numerous genes involved in DNA replication, thus playing a role in the G1 to 8 transition in the cell cycle. Do, also called DRTF (differentiation regulated transcription factor 1) has been shown to form specific multiprotein complexes with the retinoblastoma susceptibility protein, plo7, cyclins and cdk2. The DP polynuclecide was used to produce a transgenic plant. The DP nucleic and proteins are useful for increasing transformation efficiency in plants by increasing the number of dividing cells in the plant (dividing cells may be more receptive to
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                                                                                                                                                                                                      DP polypeptide; transcription factor; gene transcription; cell cycle; DNA replication; DRTF; differentiation-regulated transcription factor 1; transgenic plant; transformation efficiency; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic plants comprising an expression cassette consisting of a DP nucleic acid, when expressed, the nucleic acid increases the efficiency of plant cell transformation by increasing the number of dividing cells in the plant.
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                                                                                                                                                          DNA encoding a transcription factor designated DP
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Acosta JAT,

Veylder L,

De D

CROPDESIGN NV. Boudolf V,

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The invention relates to a novel cell cycle protein (CCP) and the compound which modulates the activity of the polypeptide and which binds to the polypeptide and anti-CCP antibody is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and anti-CCP antibody is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliand, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat to requisite the production of CCP protein or production of CCP protein forms which have decreased or obstrat activity. Compounds that bind to or modulate the activity of CCP polypeptide are useful as herbicides or plant growth regulators. The polypeptide are useful as herbicides or plant growth regulators. The polypeptide are useful for modifying cell fate, plant development, plant morphology, biochemistry and/or physiology, the length of the G1, S, G2 and/or M phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, shoot and root initiation and/or development, nodule function, dwarfism in plants, containtibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to environmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, all stress, or biotic stress such as cold, nutrient pathogenent, endoredupleate e.g. enhance crop yields, and attenuate plant quality raits, plant reproduction and seed development, endoredupleate e.g. enhance crop yields, and attenuate pathogenent, endoredupleate e.g. enhance crop yields, and attenuate plant quality traits, plant gernage cells, storage tissues and/or development, endoredupleate are protein involved in the cell cycle pathogen are correct or generate antiboddes. CCP protein is usef
                                                                                                                                                                                                         New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    occurring CCP substrates. The polynucleotide is useful for expressi protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and modulate CCP activity. The present sequence encodes a CCP protein o
                                                                                                                                                                                                                                                                                        Claim 38; Fig 39; 316pp; English.
                           12-MAY-2000; 2000US-0204045P
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        CCTACGAGCAAGAAAAAAGAAGAGGCACACGGGCAGTGGGTCCTGATAAAGGTAAACGG
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36 GlyGlyAsnAlaValGlnArgLysGly-----AlaValAspProAspLysAspArgLys
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                                                                                                                                                                                                                                                   73 -----IleValCysGluLysValGlu
Sequence 1442 BP; 451 A; 321 C; 297 G; 373 T; 0 U; 0 Other;
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                                    1442
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Cell cycle protein; CCP, ss; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield.

Arabidopsis thaliana, WO200185946-A2. 14-MAY-2001; 2001WO-IB001307

15-NOV-2001

Arabidopsis cDNA encoding cell cycle protein CCP33.

(first entry)

26-FEB-2002

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                                                                                                           155 ValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGlnGluIleGlu 174
                                                                                                                                          LysGlnPheAspAsp-----LeuGlnAsnIle 183
                                                                                                                                                                             800 GAACAAGTAATGAACATCATCGATACTCTCGGCTTATCTGCTTCCTGCCTTCAGAATCTG 859
                                                                                                                                                                                            184 LysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlylleArgLeu 202
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        AlalysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer 99
                                                                                                                                                                                                                                                                                                                                                                                                 corn; maize; cell cycle regulatory protein; transcription factor;
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                                                    560 CCAAATAACGATGGAACATCCCCTGATCAGCAACAGTATGATGAGAAAAACATAAGACGA
                                                                             GlnGlyPheAspGluLysAsnIleArgArg
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herbicide;
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This is the nucleotide sequence of a contig assembled from the CDNA inserts in clones p0005.cbmfh22r, cdelc.pk001.j13 and cen3n.pk0183.bi. It encodes a portion (see AAY32164) of a corn protein that shows homology to human cell cycle regulatory protein DP-2. The deduced amino acid sequence of this cDNA represents 50% of the middle region of the DP-2 protein. The coff contact of this cDNA represents 50% of the middle region of the DP-2 protein. The contact of the analysis of the middle region of the DP-2 protein. The contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the chimeric gene encoding all or a portion of the contact of the chimeric gene regults in product on of altered levels of the cell cycle regulatory protein, in sense or antisense ortentation, where cycle regulatory protein, in sense or antisense of cell cycle regulatory protein in a transformed host cell. The nucleic contact in plants, provide genetic tools to enhance cell growth in cycle regulation in plants, provide genetic tools to enhance cell growth in transformations. The proteins may also provide targets to facilitate contact of design and/or identification of cell cycle regulations. The proteins may also provide targets to facilitate contact of design and/or identification of cell cycle regulatory proteins may also provide targets to facilitate contact of design and/or identification of cell cycle regulatory proteins that may contact of the useful as herbicides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
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                                                         Plant-derived cell cycle regulatory proteins.
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                                                                                                                  Claim 12; Page 41; 44pp; English
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P-PSDB; AAY32164
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plant morphology, biochemistry and/or physiology, the length of the G1, S G2 and/or M phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, seed size, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, nodule function, dwarfism in plants, senescence, tolerance or resistence to stress. CCP, the polyvucteotide and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to protein levels or activity of a protein involved in the cell cycle due to convironmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as cold, nutrient cell plant activity traits, plant reproduction and seed development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally occurring CCP substrates. The polynucleoside is useful for expressing CCP protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence encodes a CCP protein of the

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219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell cycle protein; CCP; ss; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACTCATACGTCCTAAAAGAAATGCGATTCTGTGGAAGAAGAACAACATGACAGCACTCAA 743
                                                                                                                                                                                                       444 GGTAGAATTGAGAAGAAGAGTGTTTACTTACAGGAGCTACAAGATCAATATGTAGGTTTG
                                                                                                IleArgLeuProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIle
                                                                                                                                                                                                                                                                                      SerAspAspSerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAsp
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                                                      GlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis cDNA encoding partial cell cycle protein CCP16.
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744 GAGTCGATATCAAATGGAGGTGAGAGCTCA 773
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Sequence 1114 BP; 378 A; 197 C; 243 G; 296 T; 0 U; 0 Other;

nvention

211 113 331 133 391 173 631 |||:::||||||| 92 GTGAGAAGGAAATTGATTGTTGATGATTGTGAAATTGGATCAGAGAAAGGGCAA 151 271 134 LysGluileArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLysLeuGlu 153 392 AAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGAAGTCAAG 451 79 66 114 ArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLys 154 GluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGlnGluIle ||| ::::|| || || 452 ATGGATCGTAAAAGATGTGCAAAAGAAGGCTGCTTTTCTTAAAGAGTTG 40 valGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAlaAla 60 ProArglleThrGlyTrpGlyLeuArgGluTyrSerLyBlleValCyBGluLyBValGlu 80 AlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer 212 GCCAAGAAGATAACTACTACAAGGAGGTTGCAGACGAAATTATTTTTGCCACA -----GlyPheAspGluLysAsnIleArg 174 GluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSer 194 AlaGluAsn---ValAsnGlyIleArgleuProPheValLeuValLysThrSerArgLys 213 AlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPheAsnGly 1114 88 49 69 7 233 AlaProPheThrLeuHisAspAspLeuSerIleLeuGlu 245 Length: Matches: Conservative: Mismatches: Indels: Gaps: US-10-088-830-2 (1-261) x AAS96287 (1-1114) 100 MetAlaHisIleGlyGln----2.77e-33 428.50 64.32% 41.31% Similarity: Percent Similarity: Alignment Scores: Query Match: Best Local 셤 셤 ò g a d ò ò ò 셤 Š ઠ à 엄 ð 셤 8 g ò ద 8

The invention relates to a novel cell cycle protein (CCP) and the polynucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell card of company affaits, oilseed rape, soybean, sunflower and canola. CCP uncleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polypeptide are useful as herbicides or plant growth regulators. The polymentide is useful for modifying cell fate, plant development,

New cell cycle protein and nucleic acid molecule encoding it useful fregulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.

Claim 38; Fig 16; 316pp; English

Ζ; Magyar

Acosta JAT,

Veylder L,

Be

Boudolf V,

Inze D,

WPI; 2002-062249/08. P-PSDB; AAU72497

(CROP-) CROPDESIGN NV.

14-MAY-2001; 2001WO-IB001307 12-MAY-2000; 2000US-0204045P

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692 ACACCTTTCTCGGTCCATGATGATGCTTACATTTTGAAA 730

Search completed: February 6, 2005, 22:04:22 Job time : 588 secs

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Sequence:

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OSIFCC003026 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
CL9559517.1 GI:52373702
GSSS.
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza.

1 (bases 1 to 1119)
Ma.L., Wango,J., Chiu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Nong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
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Department of Bioinformatic
Beijing Institute of Genomics
Reijing Institute of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
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-USB=EST -QFWT=fastap -SUFFTX=p2n.rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDEXT=7
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CR282243 CR289243 CR246496 AF53-Rpf
BE456002 HYSMEG001
CA078334 SCRLAM100
BE511883 946064A10
CF48481 POLI 25 C
CA290160 SCAGFL801
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             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                      - nucleic search, using frame_plus_p2n model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Jatabase :

Š. Result

BQ945665 AGENCOURT BM925294 AGENCOURT

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952 ATCAAGACATCCCGAAAAGCAAGGGTGGAAATTGAGATTTCGGAAGATTCAAAGTTTGCA 1011
                                                                                                                                         227 HisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGly 246
                                                                                                                                                                                                                                                                                 CD882927 649 bp mRNA linear EST 14-JUL-2003 F1.111L02F010430 F1 Triticum aestivum cDNA clone F1111L02, mRNA
                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant genomics
                                               207 VallygThrSerArgLygAlaArgValGlu1leGlu1leSerAgpAgpSerLygPheAla
    832 AAGAAGCTTCTCCAGGAAATTGAAAAGCAGTTTGATGACCTTCAGAATATTACATTACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AsnileArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoplante, a major partnership french program in Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 31 1 69 47 54 00
Fax: 33 1 69 47 54 10
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44
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62
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum (bread wheat)
Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheAspGluLysAsnIleArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeu 126
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                                                                                                                                                                                                                                                                                                                                                  121 CCCTGTACTTCTGATTCCTTTGCTCCAATCTCTAGGGAAGGGGACGATATTCCCCCCCAA 180
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                              E
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/note="Oryza sativa exon trapped genomic sequences
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Matches:
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CA764996

AF53-Rpf 05 M03 T7 008 abl IRRI brought Stress Panicle Library oryza sativa" (indica cultivar-group) cDNA clone C0001827 5' similar to Transcription factor DP-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1), mRNA sequence.
CA764996.

EST.
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Garmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza.
1 (bases 1 to 765)
Bennett, J., Arumugam, K., Lafitte, R., Wen, J., Rudd, S. and
Bruskiewich, R.M.
Bruskiewich, R.M.
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                    130 AlaLysGluLysLysGluLleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIle 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 LeuGlnGluileGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThr 189
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Email: r.bruskiewich@cgiar.org
Email: r.bruskiewich@cgiar.org
http://www.iris.irri.org): D0201826
Assignment of putative function to the sequence by S. Rudd of the
                                                                                                61
                                               182 GCAAAAGATAAAAAGGAGATAAAGTGGATGGGCCTTACTAATTATAGATACGAAAAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Dec 2, 2002 this sequence version replaced gi:25994251.
Contact: Richard Bruskiewich
Contact: Richard Bruskiewich
Indernational Rice Research Institute
DAPO 7777, Metro Manila, Philippines
Tel: +63-2-845-0563
    US-10-088-830-2 (1-261) x CR289243 (1-612)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR289243 Oryza sativa library (Han B) Oryza sativa CDNA clone p704a10p5, mRNA sequence.
                                                                                                                                                                                                                                                                    210
                                                                                                                                                                                                                                                                                                                                                                230
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnGlyAlaProPheThrLeutisAspAspLeuSerIleLeuGluGlyValArgArgAsn 250
                                                                                                                                                                   GlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeu 190
                                                                                                                       241
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                                                                                                                                                                                                                                                                                                                                                                                                CAGGAAATCGAAAAACAGTTGGATGATCTCCAAAAACATCATGTTACGTAACCAAACACTG
                                                                       LysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeu
                                                                                                   GluSerSerAlaGluAsnValAsnGlyIleArgLeuProPheValLeuValLysThrSer
                                                                                                                                                                                                                                                                                                       302 GAAAGCTCAGCAGAGAATGTTAATGGCATCCGCCTTCCATTCGTATGGGTCAAGACATCT
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/mol_type="mRNA"
/mol_type="mRNA"
/do_xref="taxon:4530"
/clone="p704al0p5"
/clone_lib="Oryza sativa library (Han B)"
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 AGCATAGGAAGACTGGCCGCGCCCACCCTTCAC 514
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Location/Qualifiers
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AUTHORS
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CR289243
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US-10-088-830-2 (1-261) x BE456002 (1-607)
BE456002.3 GI:16318905
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                                                                                                                                                   /db_xref="taxxxn:39946"
/clone="C0001827"
/tissue_type="Penicles"
/dev_stage="Flowering"
/dev_stage="Flowering"
/clone lib="IRRI Drought Stress Panicle Library"
/note="Vector: pBluescript II SK+; Water stress was applied by not watering for 4 consecutive days. Panicles were collected from control (well watered) and stressed plants at 2 days before heading, at heading, 50% flowering and 4 days after 50% flowering."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVSMEG0019D17f Hordeum vulgare pre-anthesis spike EST 22-OCT-2001 HVSMEG0019D17f Hordeum vulgare pre-anthesis spike EST library HVSDMA0008 (white to yellow anther) Hordeum vulgare subsp. vulgare EDNA clone HVSMEG0019D17f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysGluIleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLysLeuGlu 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AAGGAGATAAAGTGGATGGGCCTTACTAATTATAGATACGAAAAGATACAGAAGTTGGAG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 AGGGGGGAAATTGAGATTTCGGAAGATTCAAAGTTTGCACGGTTCGACTTCAACGGGGGA 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGAGGCTATATGATGCTTTCAATGTGCTCATTGCAATTCGTGTTATTGCAAAAGATAAA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 ArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPheAsnGlyAla 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 TyrSerGluLeuLysSerMetAlaHisIleGlyGlnGlyPheAspGluLysAsnIleArg 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 GAAAAGCAGTTTGATGACCTTCAGAATATTACATTACGCAACCAAGCTAGTCAGAGGCCA
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    .765
    forganism="Oryza sativa (indica cultivar-group)"
/mol type="mmNa"
/culTivar="IR64"

  Munich Information Center for Protein Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                 765
125
21
17
0
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Matches:
Conservative:
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                  (http://mips.gsf.de)
Plate: 05 row: M column: 03.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             2.15e-62
651.00
89.57%
76.69%
49.36%
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BE456002
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/ Organism="Nordeum Yulgare subsp. Yulgare"
// ford type="mrkNa"
// sub species="vulgare"
// sub species="vulgare"
// db xref='taxon:112509"
// clone="HVSMEg0019D17f"
// tissue_type="pre-anthesis spike"
// lab_host="SOLR"
// lab_host="SOLR"
// lab_host="SOLR"
// lab_host="SOLR"
// lab_host="SOLR"
// lab_host="SOLR"
// lone lib="Hordeum vulgare pre-anthesis spike EST library
// hote="Vector: lambdaZAP; Site=1: EcoR1; Site 2: Xho1;
// hote="Vector: lambdaZAP; Site=1: EcoR1; Site 2: Xho1;
// hote="Vector: lambdaZAP; Site=1: EcoR1; Site 2: Xho1;
// hote="Vector: lambdaZAP; Site=1: EcoR1; Site 2: Xho1;
// hote="Vector: lambdaZAP; Site=1: EcoR1; Site 2: Xho1;
// hote="Vector: lambdaZAP; Site=1: EcoR1; Site 2: Xho1;
// hote="Vector: lambdaZAP; Site=1: EcoR1; Site 2: Xho1;
// plants were grown in the greenhouse at the University of callifornia, Riverside from each pool, equal quantities of all three RNA was preparations of the Totor of Callifornia, Riverside
// phagemids were plated and picked at the Clemson University Genomics Institute (CUG1) (Begum, Palmer, Frisch, Atkins and Wing) Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUG1 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main): The Sequence has been trimmed to remove vector sequence analysis see hitto://www.genome. To order http://www.genome. To order http://www.genome.
                                                               Hordeum vulgare subsp. vulgare
bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooldeae, Triticeae, Hordeum.
                                                                                                                                                                                               1 (bases 1 to 607)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
Fenton,R.D., Close,J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofe A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
On Jul 26, 2000 this sequence version replaced gi:13155022.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
It 0 Ordan Hall, Clemson, SC 29634, USA
Fax: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Hordeum vulgare subsp. vulgare"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total hq bases = 141
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 585.
Location/Qualifiers
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EST.
Hordeum vulgare subsp. vulgare
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615.50
84.30%
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/lab host="DH10B"
/clone lib="AM1"
/clone lib="AM1"
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/note="Organ: Apical meristem and tissues surrounding of mature plants, Vector: pSport1; Site_1: Sal1; Site_2: Mot1; An unidirectional cDNA library generated from fApical meristem and tissues surrounding of mature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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357 AAG---CTGACTCTTATTGGTCAAGAGTTTGAAGAAGAATATCAGGAGGAGGAGTGTAT 413
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Indels:
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA078334 665 bp mRNA linear EST 23-SEP-2003 SCRLAM1006A02.g AM1 Saccharum officinarum cDNA clone SCRLAM1006A02 5', mRNA sequence.
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                                                                                         ValHisileLeuGluAlaSerSerValProProLeuProGlu---AlaGlyGlyAsnAla 39
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Clone dietribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
                                                                                                              ProArg1leThrGlyTrpGlyLeuArgGluTyrSerLys1leValCysGluLysValGlu
                     MetAlaProProArgGlyGlyAlaAlaAlaAlaAlaThrAlaAlaLeuAspLeuThrGly
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Caixa Poetal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 665)
Vetrore, A.L., da Silva, F.R., Kemper, E.L., the libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (Dases 1 to 548)

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                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="just after the transition from vegetative to inflorescence development"
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Maize ESTs from various cDNA libraries sequenced at Stanford
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 550 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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Conservative:
Mismatches:
Indels:
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cDNA, mRNA sequence.
                         GI:9733131
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575.50
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Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 634)

2 Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Eastman, A. and Pratt, L.H.

An EST database from Sorghum: pollen
Unpublished (2003)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
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/lab_host="bHi0B-T1" phage-resistant E. coli"
/clone=lb="bollen"
/clone=lb="pollen"
/clon
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Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science: plant material and RNA prepared at Texas A & M University,
Science: plant material aboxatory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
sculude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
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291 ACTCTTATTGGTCAAGAGTTTGATGAGAAGAATATCAGGAGGAGAGAGTGTATGATGCTTTT 350
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POLI_25_C08.gl_A002 Pollen Sorghum bicolor cDNA clone
POLI_25_C08_A002 5', mRNA sequence.
CP4844481
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Sorghum bicolor
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ò 셤 õ 셤 ò 셤 8 셤 ò 요 ò 셤 8 셤 8 셤 ò 유 8

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/note=Torgan: Developing inflorescence and rachis /note=Torgan: Developing inflorescence and rachis (10cm-long); Vector: pSport!; Site 1: Sall; Site 2: Not!; An unidirectional cDNA library generated from [Developing inflorescence and rachis (10cm-long)]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                      be found
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Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br
Clone distribution: clone distribution information can be through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 013 row: C column: 10
Seq primer: 77 Promoter Primer.
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120
23
44
44
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                                                                                                                                                                                                                                                                                                /clone="SCAGFL8013C10"
/lab_host="DH10B"
/clone_lib="FL8"
                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:4547"
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SCAGFL8013C10.g FL8 Saccharum officinarum cDNA clone SCAGFL8013C10
5', mRNA sequence.
CA290160
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
                                                                                                                                                                                                                                                                                                                                    21 ValHisileLeuGluAlaSerSerValProProLeuPro----
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Conservative:
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KEYWORDS
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77

466

16

526

96

586 111 646 131 706 151

-GlnGlyPheAspGluLysAsn

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BX831357.1 GI:42454999
HTC; GSLT CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 bases 1 to 1418)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluileGluLysGlnPheAspAspLeuGlnAsnileLysLeuArgAsnGlnThrLeuGlu 191
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                                                                                                                                                  GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys
                                                                                                                                                                                          107 GGTGATGATGCTGGTTCTCAAGGAGCTTCTGGTGTTAAGAAGAAGAAGAAGAGGGGGACAGCGT
                                                                                                                                                                                                                                    57 AlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGlu
                                                                                                                                                                                                                                                           LysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 SerSerAlaGluAsnValAsn---GlyIleArgLeuProPheValLeuValLysThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 ArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lastelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Craud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weisenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                          542
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                                                                                    SerAsnTyrArgTyrGluLysIleLysLysLeuGluGluValArgLysGluLeuValAsn 161
                                                                                                                                                                                               162 LysileArgAsnLysLysAlaLeuLeuGln-GluIleGlu-LysGlnPheAspAspLeuG 181
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The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castell V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrasic payer.
                        ValleuileAlaLeuArgValileAlaLysGluLysLysGluIleArgTrpMetGlyLeu
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/plasmid="pCMVSPORT_6"
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Matches:
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HTC, GSLT. CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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2 (bases 1 to 1403)
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Pred. No.:
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The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein http://www.genoscope.cns.ff/externe/sequences/Banque_Projet_EF/Full
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                                                   CNSO9ZIR

Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS73ZB01 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
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                         192 SerSerAlaGluAsnValAsn---GlyIleArgLeuPro-PheValLeuValLysThrSe 210
                                                                                                                                           210 rArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPh
                                                                                                                                                                                                                                 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
                                                                                                                                                                                                     230 eAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
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BX831265.1 GI:42456015
HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                     Direct Submission

Listed (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

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URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 LeuLysSerMetAlaHisIleGly------GlnGlyPheAspGluLysAsn 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 ileArgArgArgValTyrAspAlaPheAsnValLeulleAlaLeuArgValileAlaLys 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys
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    1418
    organism="Arabidopsis thaliana"

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CK278661 592 bp mRNA linear EST 03-AUG-2004 EST724739 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAE738 5' end, mRNA sequence.
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Solanum tuberosum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
asterids, lamides, Solanales, Solanaceae, Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           211 TTCAT-GTGCTCATTGCAATTCGTGTTATTGCAAAAGATAAAAAGGATATAAAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::
151 ATTACGCAGAACGGTCTGGAGTTTGATGAGAAGAATATTAGGCGGAGGGTATATATGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GGCCTTACTAATTATAGATACGAAAAGATACAGAAGTTGGAGGAAGTTCACAAAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 uValAsnLysileArgAsnLysLysAlaLeuLeuGlnGluIleGlu-LysGlnPheAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 CATCACCAGGATCCAGAATAAGAAAAGCTTCTCCCAGAAATTGAATACGCAGATTGATG
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20
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8
8
Email: bhan@ncgr.ac.cn
Clone requests: bhan@ncgr.ac.cn
This is rice cdna est clone
Web site: http://www.ncgr.ac.cn.
Location/Qualifiers
ce 1...70
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/ mol_type="mRNA"
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/ clone="py30d01p5"
/ clone="lib="Oryza sativa library (Ha
                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
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EST.
                                                                                                                                                                                                                             8.53e-42
467.00
78.92%
66.87%
35.41%
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E han, E. to 702)

S Han, B., Feng, Q., Huang, Y.C., Ying, K., Li, Y., Guan, J.P., Zhu, J.J., Weng, Q.J., Zhang, Y.L., Mu, Y.L., Mu, Z., Chen, L., Fan, D.L., Weng, Q.J., Lu, Y., Li, Y., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, Chen, W., Wu, S.A. and Xue, Y.B.

Rice cDnA EST clone
Unpublished (2003)

Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 200233, China
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GAACTGGAAGAACAATATGTAGGCCTTCAGAATCTTGATACAGAGAAATGAGCACTTATA 929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlulleGluLysGlnPheAspAspLeuGlnAsnIleLysLeu-ArgAsnGlnThrLeuGl 191
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|TAAAAGAACGAACGACTCTCACTTAGGAACAGAATTGAGAAGAAAACTGCATATTCCCAA
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                                                                     GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys
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        Gaps:
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Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones,
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Lowa State, then clones may be requested from ZmDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTC 16-OCT-2002
  413 AAGAAACAGCCTATTTAGAAGAACTTGAAGATCAATATGTAGGGCTTCAAAACCTCATA 472
                                                                                                                                                                                                                                                                                                                                      532
                                                                                 145 ArgTyrGluLyBileLyBLyBLeuGluGluValArgLysGluLeuValAsnLyBileArg 164
                                                                                                                                                                                   165 AsnLysLysAlaLeuLeuGlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLys 184
                                                                                                                                                                                                                                                                                                                                                                                      204 PheValLeuValLysThrSerArgLysAlaArgValGluIleGluIleSerAspAspSer 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 LysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIle 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      593 CAGCTGGTGCATTTCGACTTCAACAGCACTCCGTTTGAGCTACATGACGATAATTATATC 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

( Cases 1 to 1245)
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                                                                                                                                                                                                                                                                                                                                                                                                                353 GATGCAAATGATATTGAGGAGCTAAAGACTGAGCGTCTTAACTTGAGAAATAGGATTGAA
                                                                                                                                                                                                                                                                                    185 LeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlyIleArgLeuPro
                                                                                                                                                                                                                                                                                                                                 473 AAACGCAATGATCAGTTGTATGGCTCAGGCAATGCTCCTAGTGGTGTGGTGTGGCTTTACCG
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Library"
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/db_xref="MaizeDB:634768"
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Coe, E.H.
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Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="PODE738"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab.bost="NH10B-TonA"
/lab.bost="NH10B-TonA"
/clone lib="potato abiotic stress cDNA library"
/clone lib="potato abiotic stress cDNA library"
/clone lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site_1: ECORI; Site_2: NotI;
supplier: Solanum tubersoum var. Kennebec plants were
grown from cuttings on a labr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants: Set 1 involved saturation of
the soil with 150 mm NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 14h, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PheAspGluLysAsnIleArgArgArgValTyrAspAlaPheAsnValLeuIle 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AAACAATATGATGAGGAAGAACATCAGACGAGGGGTCTACGATGCTCTGAACGTACTTATG 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                             Bmail: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 TyrSerLyslleValCysGluLysValGluAlaLysGlyArgThrThrTyrAsnGluVal
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  Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B. Generation of ESTs from abiotic stressed potato tissue Unpublished (2003)
Other ESTs: EST724740
Contact: Robin Buell
The Institute for Genomic Research
                                                                                                                                                      9712 Medical Center Dr, Rockville, MD 20850, USA
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Mismatches:
Indels:
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/cultivar="Kennebec"
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9
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                83 ArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSerMetAlaHis 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluGluValArgLysGluLeuVal-----AsnLysIleArgAsnLysLysAlaLeu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrSerArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPhe 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 GluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTICAATAGCACCCCATICGAGCTGCACGACTCATACGTCCTAAAAGAAATGCGA 717
                                                                                                                                                                                -----GACGACGCCCCCTCGTCGCAGCTCCTACGAGCAAGAAGAAAGGAGAGAGC 102
                                                                                                                                                                                                                                                                                                                                           -------IleGlyGlnGlyPheAspGluLysAsnIle 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 AAAAAGGAGATCCAGTGGAAGGGCTTGCCGCGT-----ACTAGTATAAGTGACATT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ArgAsnSerileGlyArgAlaGlyArgAla 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::: ||||||
118 TTCTGTGGAAGAGAACAACATGACAGCACTCAAGAGTCGATATCAAATGGAGGTGAGAGC 777
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                                                                                                                                                                                                                      ArgGlyGlyAlaAlaAlaAlaThrAlaAlaLeuAspLeuThrGlyValHisIleLeu
                                                                                                                                                           GlualaSerSerValProProLeuProGlualaGlyGlyAsnAlaValGlnArgLysGly
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           Length:
Matches:
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
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Sequence 3, Appli
                                                                        February 6, 2005, 21:42:57; Search time 196 Seconds (without alignments) 2178.920 Million cell updates/sec
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Sequence 7,
Sequence 1,
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/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-723-415B-5
US-09-189-627A-5
US-09-710-861-5
US-09-710-861-5
US-09-189-627A-7
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US-09-189-627A-1
US-09-189-627A-1
US-09-189-61-3349
US-09-723-415B-3
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Delop 6.0 ,
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Sequence 465, App
Sequence 120497,
Sequence 120497,
Sequence 12091, A
Sequence 14679, A
Sequence 105247,
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1, Appli
1, Appli
12, Appl
12, Appl
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             Sequence 1, Appli
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Sequence 1, Appli
                              Sequence 1399,
Sequence 2937,
Sequence 566,
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US-09-640-211A-465
US-09-640-211A-465
US-09-640-211A-467
US-09-949-016-120491
US-09-949-016-15091
US-09-949-016-1679
US-09-949-016-1679
US-09-949-016-105247
US-09-242-737-1
US-08-242-711-1
US-08-462-174-1
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US-08-462-174-1
US-08-462-174-1
US-08-462-174-1
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                               US-09-949-016-4380
US-08-139-937-13
US-09-023-655-1230
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSES: INCYTE PHARMACEUTICALS, INC.
STREET: PALO ALTO
CTTY: PALO ALTO
COUTRY: USA
                                                                                                                                                                   PCT-US93-11310-13
US-08-306-691B-18
                                                                                                                                                                                              US-08-801-092-2
US-09-517-584A-3
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US-08-481-814A-1
                                                                                                                                                                                                                                                         US-09-023-655-1456; Sequence 1456, Application US/09023655; Patent No. 6607879
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918 ATGTCGTTTGGCCTGGAGTCAGGCAAATGCTCTCTG 953
                                                         ; Sequence 5, Application US/08723415B; Patent No. 5859199; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 1157 base pairs TYPE: mucleic acid STRANDEDNES: single
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37.30%
29.53%
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LOCATION: 1..1
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Pred. No.:
                                            JS-08-723-415B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 GluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
                                                                                                                                                                                                                                                                                                                                                                                                                                   327 AAAGGAGATAAA---AATGGGAAAGGCTTGAGACACTTTTCAATGAAAGTGTGTGAGAAA 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 ArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLys 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 GluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGlnGluIle 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 GluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSer 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 AlaGluAsnVal------AsnGlyIleArgleuProPheValLeuValLysThr 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 SerArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHis---Phe 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      861 AATTTTGACAACACC---TTTGAGATCCATGATGACATAGAAGTACTAAAAGGGGATGGGA 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564 AAAGAAATCAAGTGGATTGGCCTGCCTACCAATTCTGCTCAGGAATGTCAGAATCTGGAG 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 AlaAlaProArglleThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGluLys
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Matches:
Conservative:
Mismatches:
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         TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 14;
SEQUENCE CHARACTERISTICS:
LENGTH: 2320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
(650) 855-0555
                                                                                                                                                                                                                             399.50
58.33%
37.30%
30.29%
                                                                                                      TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                  CLONE: 9604478
US-09-023-655-1456
                                                                                                                                                                                                  Alignment Scores:
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APPLICANT: LaThangue, Nicholas B.
APPLICANT: LaThangue, Nicholas B.
APPLICANT: delaluna, Susana
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES: NICHOR & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                           ALDKESSEE: NIANON & VANDERGIE F.C.

CITY: Arlington
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN PC-DOS/MS-DOS
SOFTWARE: PATCHIN PC-DOS/MS-DOS
SOFTWARE: PATCHIN PC-DOS/MS-DOS
SOFTWARE: PATCHIN PC-DOS/MS-DOS
SOFTWARE: PATCHIN DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 13-SEP-1996
CLASSIFICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
REFERRINGE/DOCKET NUMBER: 25,327
REFERRINGE/DOCKET NUMBER: 25,327
REFERRINGE/DOCKET NUMBER: 117-220
TELEFRAX: 703-816-4100
TELEFRAX: 703-816-4100
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316 CGAAGAGTTTATGATGCTTTAAATGTACTAATGGCGATGAACATAATTCAAAGGAAAAA 375
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                                    18 LeuThrGlyValHisIleLeuGluAlaSerSerValProProLeuProGluAlaGlyGly 37
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                                                                                                        38 AsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAla
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APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REPERBNCE: 620-54
CURRENT APPLICATION NUMBER: US/09/110,861
CURRENT PELLING DATE: 1090-11-13
PRIOR PILLING DATE: 1998-11-10
PRIOR FILLING DATE: 1996-10-30
PRIOR FILLING DATE: 1996-10-30
PRIOR FILLING DATE: 1996-09-30
PRIOR FILLING DATE: 1996-09-30
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6387649
GENERAL INFORMATION:
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114 ArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLys
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                                                   LysSer------MetAlaHisIleGlyGlnGlyPheAspGluLysAsnIleArg
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Patent No. 6159691
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APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana
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Best Local Similarity:
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ORGANISM: mouse
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SEQ ID NO 5
LENGTH: 1157
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US-09-189-627A-5
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Matches:
Conservative:
Mismatches:
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LOCATION: (1)..(1110)
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Best Local Similarity:
                           TYPE: DNA ORGANISM: mouse
                                                                                                                       Alignment Scores:
SEQ ID NO 5
LENGTH: 1157
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Sequence 7, Application US/08723415B
Fatent No. 5859199
GENERAL INFORMATION:
APPLICANT: Larbangue, Nicholas B.
APPLICANT: Galaluna, Susana
TITLE OF INVENTION: THARBOF
TITLE OF INVENTION: THARBOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
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ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: FILIDPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
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Mismatches:
Indels:
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CIASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9610195.1
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: CTAMFORMATION:
REFERENCE/DOCKET NUMBER: 117-220
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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RESULT 5 US-08-723-415B-7

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GluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLys 151
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595 CAACAAAACCAGGGCCCTCCAGCTGTGAATTCCACCATTCAGCTGCCATTTATAAATCATT
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                                   IleArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLys
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APPLICANT: de la Luna, Susana
APLICANT: de la Luna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT PILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1996-09-30
PRIOR PILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
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ORGANISM: mouse
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-GCTGGCTGG 117
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                                                     38 AsnAlaValGlnArgLysGlyAla-----ValAspProAspLysAspArgLysLys
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parent No. 6387649
general incombarion us/09710861
parent No. 6387649
general incombarion:
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APPLICANT: La Thangue, Nicholas
i APPLICANT: La Thangue, Nicholas
i APPLICANT: La Thangue, Nicholas
i TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189, 627
FRICH APPLICATION NUMBER: US/09/189, 627
PRIOR APPLICATION NUMBER: 08/723, 415
PRIOR APPLICATION NUMBER: 08/723, 415
PRIOR FILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
IENGTH: 1202
TYPE: DNA
CREATION NOBE
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| GAACTTCTCCTTCAGCAAATTGCTTTTAAAAACCTGGTACAGAGAAATCGACAAAATGAA 594
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; NAME/KEY: CDS
; LOCATION: (1)..(1155)
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95 SerGluLeu---LysSerMetAlaHisIleGly-----GlnGlyPheAspGluLysAsn 111
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                     TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
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98
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86
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRING APPLICATION DATA:

APPLICATION NUMBER: US/08/723,415B

FILING DATE: 30-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9610195.1

FILING DATE: 15-MAY-1996

ATORNEY/AGENT INFORMATION:

NAME: CTEAMFORD, Arthur R.

REGISTRATION NUMBER: 25,327
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                            3: NIXON & VANDERHYE P.C.
1100 No. 5859199th Glebe Rd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 11'
TELECOMMUNICATION: TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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57.48%
38.58%
29.49%
                TITLE OF INVENTION: TRAMITION OF TITLE OF INVENTION: THEN NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSEE: NIXON & VANSTREET: 1100 No. 58591
deLaluna,
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MOLECULE TYPE: cDNA
                                                                                                                                                       CITY: Arlington
STATE: VA
COUNTRY: USA
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Query Match:
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LOCATION:
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Sequence 1, Application US/08723415B Patent No. 5859199 GENERAL INFORMATION: APPLICANT: LaThangue, Nicholas B.

US-08-723-415B-1

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                                                                                                         361 CGAAGCAAAAAGGAGATAAA---AATGGGAAAGGCTTGAGACATTTTTCAATGAAGGTG
                                                                                                                                                            CysGluLysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyr
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                                                          55 GluLysAlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIleVal
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TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-64
CURRENT APPLICATION NUMBER: US/09/180,627
CURRENT FILING DATE: 2000-11-13
FRIOR PAPLICATION NUMBER: US/09/189,627
FRIOR PELLOR DATE: 1998-11-10
FRIOR PELLOR DATE: 1998-11-10
FRIOR APPLICATION NUMBER: US/02.30
FRIOR FILING DATE: 1996-05-15
FRIOR FILING DATE: 1996-05-15
FRIOR FILING DATE: 1996-05-15
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Patent No. 6387649
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
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; LOCATION: (1)..(1338)
US-09-710-861-1
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ORGANISM: mouse
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US-09-710-861-1
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228 ---PheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGly 246
                                                                                                            LeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGln 171
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CURRENT APPLICATION NUMBER: US/09/189, 627A
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR PILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SSOFTWARE: PATENTIN Ver. 2.0
SSOFTWARE: PATENTIN Ver. 2.0
LENGTH: 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 ValArgArgAsnSerIleGlyArgAlaGlyArgAlaThrLeu 260
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Conservative:
Mismatches:
Indels:
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GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas APPLICANT: de la Luna, Susana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7e-38
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LOCATION: (1)..(1338)
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Best Local Similarity:
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ORGANISM: mouse
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US-09-189-627A-1
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RESULT 11
US-09-949-016-3349
Sequence 3349, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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| GAACTICTCCTTCAGCAAATIGCTTTTAAAAACCTGGTACAGAGAAATCGACAAAATGAA 777
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                                                                                                                                       LeuThrGlyValHisIleLeuGluAlaSerSerValProProLeuProGluAlaGlyGly 37
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GTCACTCAGACTCACATAGCTGAGGCT--------GCTGGCTGG
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                                     Conservative:
Mismatches:
Indels:
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           Length:
Matches:
          5.7e-38
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                                     Percent Similarity:
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Alignment Scores:
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396 TCAGAAAGTAAACGAAGGAAAAAAGGAGATAAA---AATGGGAAAGGCTTGAGACACTTT
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930 AAGTTTGAGTATCTTTTCAATTTTGACAACACC---TTTGAGATCCATGATGACATAGAA
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Matches:
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Mismatches:
Indels:
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         PRIOR PAPLICATION NUMBER: 60/21,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3349
LENGTH: 1427
TYPE: DNA
TYPE: DNA
US-09-949-016-3349
2000-04-14
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GlulleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLyslleLysLysLysLeuGluGlu 154
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                    115 ArgValTyrAspAlaPheAsnValLeulleAlaLeuArgValIleAlaLysGluLysLys
                                                                                         175 LysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSerAla
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; Sequence 3, Application US/09189627A
; Patent No. 6159691
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas
; APPLICANT: de la Luna, Susana
; TITLE OF INVENTION: TRANSCRIFTION FACTOR DP-3 AND ISOFORMS THEREOF
; FILE REFERENCE: 620-627A
; CURRENT APPLICATION NUMBER: US/09/189,627A
; CURRENT FILING DATE: 1998-11-10
; FRIOR PEPLICATION NUMBER: 08/723,415
; PRIOR FILING DATE: 1996-09-30
; PRIOR FILING DATE: 1996-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PATENTIN VET. 2.0
; SEQ ID NO 3;
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ORGANISM: mouse
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LOCATION: (1)
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Patent No. 5859199
CENEAL INFORMATION:
CENEAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: deLaluna, Susana
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1154
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Mismatches:
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Gaps:
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Matches:
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STREET: 1100 No. 5859199th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                           CURKEN' AFFLICATION NUMBER: US/08/723,415B
PILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY,AGENT INFORMATION:
NAME: CTAMFORD ATTON:
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-816-4000
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                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1154 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Query Match:
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US-08-723-415B-3
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RESULT 15
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                                                  AsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAla 57
LeuThrGlyValHisileLeuGluAlaSerSerValProProLeuProGluAlaGlyGly 37
                                                                           AlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGluLys
                                                                                                                                                  ValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeu
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GENERAL INFORMATION:

FACENTE INFORMATION:

APPLICANT: La Thangue, Nicholas

APPLICANT: La Thangue, Nicholas

APPLICANT: La THANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF

FILE REFERENCE: 620-611-13

CURRENT APPLICATION NUMBER: US/09/110,861

CURRENT FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: US/09/189,627

PRIOR APPLICATION NUMBER: US/09/189,627

PRIOR APPLICATION NUMBER: US/09/189,627

PRIOR APPLICATION NUMBER: US/09/189,627

PRIOR APPLICATION NUMBER: GB 9610195

PRIOR APPLICATION NUMBER: GB 9610195

PRIOR APPLICATION NUMBER: GB 9610195

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PALENT NOS: 25

SOFTWARE: PALENT NOS: 25

SEQ ID NO 3

KA I LENGTH: 1154
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GTCACTCAGACTCACATAGCTGAGGCTGCT
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US-09-710-861-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                        58 AlaAlaProArglleThrGlyTrpGlyLeuArgGluTyrSerLyslleValCysGluLys
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Matches:
Conservative:
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Gaps:
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Patent No. 5863757
                                                                                                                         1.78e-37
384.00
57.37%
37.45%
29.11%
                                             US-09-710-861-3
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Best Local Similarity:
Query Match:
DB:
ORGANISM: mouse
FEATURE:
NAME/KEY: CDS
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126 LeuArgValileAlaLysGluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArg 145
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                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PetentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
APPLICATION NUMBER: US/08/428,131
APPLICATION NUMBER: S14
ATTORNEY/ABRATION STAMPORMATION:
MAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELEPHONE: (703) 816-4100
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
**NUMBER: TELEPHONE: (703) 816-4100
INFORMATION POR SEQ ID NO: 1:
**SUGUENCE CHARACTERISTICS:
**NUMBER: TELEPHONE: (703) 816-4100
**INFORMATION PASSE ID NO: 1:
**NUMBER: TELEPHONE: (703) 816-4100
**INFORMATION PASSE DAIRS
              APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STREET: U.S. 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STREET: U.S. 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STREET: U.S. 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STREET: 22201-4714
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Matches:
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378.50
62.44%
42.44%
28.70%
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TYPE: nucleic acid
STRANDEDNESS: double
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55..1284
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
GENERAL INFORMATION:
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STRANDEDNESS:
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; LOCATION:
US-08-428-131-1
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166 LysLysAlaLeuLeuGlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLysLeu 185
                                                                                                               202 LeuProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIleSerAsp 221
                                                                                                                                                                       222 AspSerLysPheAlaHis---PheGluPheAsnGlyAlaProPheThrLeuHisAspAsp 240
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-Q=/cgn2 1/USPTO spool/US10088830/runat_04022005_122604_29641/app_query.fasta_1.455
-DB==bbliahed Applications NA -QFMT=fastap -SUFPIX=plan.rinpb_MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 - MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXIEN=200000000 -USRE=10310088830 GCGN 1 1 480 Grunat 04022005_122604_29641
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NGG SCORE=0 - WAIT -DSPBLOGX=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -SCAPPOP=10 -XGAPEXT=0.5
                                                                                                                                                                                                                                                           February 6, 2005, 23:22:07; Search time 580 Seconds (without alignments) 2590.084 Million cell updates/sec
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1 MAPPRGGAAAATAALDLTG......SILEGVRNSIGRAGRATLH 261
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'(cgn2_6/ptodata/2/pubpna/USO7_PUBCCMB.seq:*
'(cgn2_6/ptodata/2/pubpna/USO6_PUBCMB.seq:*
'(cgn2_6/ptodata/2/pubpna/USO6_PUBCCMB.seq:*
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/cgnz_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                          OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		; ;
Description	Sequence 33888, A Sequence 4049, Ap Sequence 1190, Ap Sequence 1033, Ap Sequence 2033, Ap Sequence 2033, Ap Sequence 1176, Ap Sequence 1176, Ap Sequence 1176, Ap Sequence 1176, Ap Sequence 1177, Ap Sequence 1135, Ap Sequence 1357, Ap Sequence 2031, Appl Sequence 2031, Appl Sequence 2031, Appl Sequence 2031, Appl Sequence 2031, Appl Sequence 2031, Appl Sequence 234, Appl Sequence 234, Appl Sequence 234, Appl Sequence 234, Appl Sequence 234, Appl Sequence 234, Appl Sequence 234, Appl Sequence 234, Appl Sequence 124, Appl Sequence 1254, Appl Sequence 1254, Appl Sequence 1254, Appl Sequence 1254, Appl Sequence 1254, Appl Sequence 125, Appl Sequence 125, Appl Sequence 125, Appl Sequence 125, Appl Sequence 125, Appl Sequence 125, Appl Sequence 125, Appl Sequence 125, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence 27279, Appl Sequence	Associated
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Exovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated V
TITLE OF INVENTION: Plante
FILE REFERENCE: 38-21(5)3122)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 4115
LENGTH: 774
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                              CTCCAGGAAATTGAAAAGCAGTTTGATGACCTTCAGAATATTACATTACGCAACCAGGCT
                                                                                     190 LeuGluSerSerAlaGluAsnValAsnGlyIleArgLeuProPheValLeuValLysThr
                                                                                                               SerArglysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGlu
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; OTHER INFORMATION: Clone ID: MRT4577_103754C.1
US-10-425-115-4115
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Sequence 4115, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-437-963-33888
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50.41%
63.84%
LENGTH: 1406
TYPE: DNA
ORGANISM: Oryza Bativa
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Sequence 40.9. Application US/10425114

Sequence 40.9. Application US/10405114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114

FILE REFERENCE: 38-21(53113)B
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 4049
LENTH: 1350
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380 GAACTGGTTGCTGAGTTT---TCAGATCCCAATATTAATATTGACTCTCCAGATCCTGAT 436
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677 CAAAACTIGGITCGGCGAAAIGAGCAGCTATAIGGGTCAGGAGAIGCACCTTCCGGTGGA
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                                          Conservative:
Mismatches:
Indels:
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Shou Yihua
APPLICANT: Shou Yihua
APPLICANT: Can Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 43806
                                                                                                                                                                                                                                                 248
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386 GAGCTTGTTGCTGAATTTTCTGAACCAATAGTGAATTGCCCCCTGATCAGCAACAA 445
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US-10-424-599-43806
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Publication No. US20040031072A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Asso.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Asso.

FILE REFERENCE: 38-21(53222) B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 87351

LENGTH: 1585
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Conservative:
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US-10-425-115-87351
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Sequence 1176, Application US/09954456
Batent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Process
                                                                                                                                                                                                                                                                                                    266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 LysGlulleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLysLeuGlu 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 GluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSer 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 GluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   861 AATTTTGACAACACC---TTTGAGATCCATGATGACATAGAAGTACTAAAAGCGGATGGGA 917
                                                                                                                                                                                                                                                       18 LeuThrGlyValHisIleLeuGluAlaSerSerValProProLeuProGluAlaGlyGly 37
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                                                                                                                                                                                                                                                                                                                                                                            267 GATAGAAAACGGGCTAGAAATTTATAGACTCTGATTTTCAGAAAGTAAACGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 LysSer-----MetAlaHisIleGlyGlnGlyPheAspGluLysAsnIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 ACCAATTCAAATAACCATTTGGCTGCTGATTCGCAGGCTTATGATCAGAAGAACATTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 CGAAGAGTTTATGATGCTTTAAATGTGCTAATGGCAATGAACATAATTTCAAAGGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                       58 AlaAlaProArglleThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 AAAGGAGATAAA---AATGGGAAAAGGCTTGAGACACTTTTCAATGAAAGTGTGTGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624 ATAGAGAAGCAGAGGGGATAGAACGGATAAAGCAGAAGCGGGCCCAGCTGCAAGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 AlaGluAsnVal-----AsnGlyIleArgLeuProPheValLeuValLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744 AACCAGGGCCGGCGGCTCTGAACTCTACCALTCAGCTGCCALTCATAATCATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHis---Phe
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                                                                                                                                                                                                                                                                                           222 GTTACTCAGACACACATAGCAGAAGCTACTGGCTGGGTCCCT
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                                                                                                        Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
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30.29
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Best Local Similarity:
      JS-10-641-643-1456
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Pred. No.:
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                                                                           566 AATGATATTGAAGAACTAAAGACAGAGGGCTTGGGCTCAGGAATAGAATTGAAAAGAAA 625
                                                                                                                                                                      685
                                                                                                                                                                                                       gAsnGlnThrLeuGluSerSerAlaGluAsnValAsnGly---IleArgLeuProPheVa 205
                                                                                                                                                                                                                                   -TIGGTACAGACACGCCCTCATGCAACTGGGAAATATCAGAAATATGCAGACACACAGCT 804
                                                                                                                                                                                                                                                                                                                                                                              245
                                                                                                                                                                                                                                                                                                                                                                                               805 TGTTCATTTTGATTTCAATAGCACTCCTTTTGAGCTGCATGATCATTATGTTCTCAA 864
506 GATATTATTTCCAAGGACAAAAAGGAAATTCAATGGAGGGGCCTTCCTCGTACTACTGTG 565
                                                                                                                       LysAlaLeuLeuGlnGluIleGlu-LysGlnPheAspAspLeuGlnAsnIleLysLeuAr
                                                                                                                                                                                                                                                                                                                                                                       225 eAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerlleLeuGl
                                    GluLysIleLysLysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLys
                                                                                                                                            626 ACAGCCIAICIGCAGGAGCTIGAGGAAGCAATICATAGGICTICAGAACCTTAITCAACG
                                                                                                                                                                                                                                                                                     205 lieuvaliysThrSerArgLysAlaArgValGluileGiuileSerAspAspSerLysPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOSITION FOR GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1455, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Enjamin G.
Susan G. Stuart
Jeffrey J. Sellhamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACE
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1456:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1508
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: GENBANK
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APPLICANT: Schiegel, Wilson
APPLICANT: Monahan, John
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVELE
TITLE OF INVENTION: NOVELE
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMBER: 09/185,276
PRIOR FILING DATE: 2003-02-04
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-09-16
PRIOR FILING DATE: 2000-06-09-16
PRIOR FILING DATE: 2000-06-09-16
PRIOR FILING DATE: 2000-06-09-18
PRIOR FILING DATE: 2000-06-09-18
PRIOR FILING DATE: 2000-06-09-18
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER: FASSESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                211 ArgiysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHis---PheGlu 229
                   696 AGAAAAACAGTCATAGATTGCAGCATCTCCAGTGAC---AAGTTTGAGTATCTTTTCAAT 752
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                                                                                                                                 230 PheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArgArg
                                                                                                   195 GluAsnVal-----AsnGlyIleArgLeuProPheValLeuValLysThrSer
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 20983, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel. Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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Best Local Similarity:
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LENGTH: 2968
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Pred. No.:
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219 AAAGGAGATAAA---AATGGGAAAGGCTTGAGACACTTTTCAATGAAAGTGTGTGAGAAA 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LysSerMetAlaHisIleGly-----GlnGlyPheAspGluLysAsnIleArgArg 114
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Mismatches:
Indels:
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Matches:
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR PLING DATE: 2000-09-26
PRIOR PLING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
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PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
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58.17%
37.45%
29.87%
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US-09-954-456-1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-088-830-2 (1-261)
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Best Local Similarity:
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: Sequence 26827
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: Sequence 26827
: Supplication US/10357930
: Publication No. US20040259086A1
: GENERAL INFORMATION:
: APPLICANT: Endege, Wilson
: APPLICANT: Endege, Wilson
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND THERAPY OF
: TITLE OF INVENTION: HUMAN PROSTATE CANCER
: TITLE OF INVENTION: 1007BCN
: TITLE OF INVENTION: 1007BCN
: TITLE OF INVENTION: 007BCN
: TITLE OF INVENTION: 007BCN
: TITLE OF INVENTION: 007BCN
: FILE REFERENCE: MRI-007BCN
: CURRENT FILING DATE: 2003-02-04
: PRIOR PELICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
: PRIOR PELICATION NUMBER: 60/183,319
: PRIOR PELICATION NUMBER: 60/201,334
: PRIOR APPLICATION NUMBER: 60/201,334
: PRIOR PELING DATE: 2000-06-25
: PRIOR APPLICATION NUMBER: 60/211,314
: PRIOR PELING DATE: 2000-06-25
: PRIOR APPLICATION NUMBER: 60/211,314
: PRIOR APPLICATION NUMBER: 60/211,314
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| CTACAGCAAATCGCTTTCAAAAACCTGGTACAGAGAAATCGACAAAATGAGCAGCAAAAC 777
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                                                      AlaAlaProArglleThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGluLys
                                                                                                                                                            ---LysSerMetAlaHisIleGly-----GlnGlyPheAspGluLysAsnIleArgArg
                                                                                                                                                                             AsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAla
                                                                               861 AAAGGAGATAAA---AATGGGAAAGGCTTGAGACACTTTTCAATGAAAGTGTGTGAGAAA
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                 Matches:
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26827
LENGTH: 2968
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OTHER INFORMATION: n = A,T,C
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394.00
58.17%
37.45%
29.87%
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Best Local Similari
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Pred. No.:
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                                                                                                                        TYPE: DNA
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GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Town, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 17642

LENGTH: 476
                                                                                                                                       229 uPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArgAr 249
                                                                                                                                                                                                                                                                                               895 TTTTGACAACACC---TTTGAGATCCATGATGACATAGAAGTACTAAAGCGGAATGGGAAT 951
 558 AGAGAAGCAGAGGCGGATAGAACGGATAAAGCAGAAGCGGGCCCAGCTGCAAGAACTTCT 717
                                       174 uLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSerAl 194
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                                                                           718 CCTACAGCAAATCGCTTTCAAAAACCTGGTACAGAGAAATCGACAAAATGAGCAGCAAAA
                                                                                                               194 aGluAsnVal------AsnGlyileArgLeuProPheValLeuValLysThrSe
                                                                                                                                                                                           rArgiysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHis---PheGl
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Mismatches:
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Matches:
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; Publication No. US20040172684A1
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379.50
84.21%
69.30%
28.77%
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-767-701-17642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 LeuThrGlyValHisIleLeuGluAlaSerSerValProProLeuProGluAlaGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGGAGATAAA---AATGGGAAAGGCTTGAGACACTTTTCAATGAAAGTGTGTGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLysLy
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                                                                                                                                                                                                         APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR PPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
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GTTACTCAGACACACATAGCAGAAAGCTACTGGGTCCCT
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Mismatches:
Indels:
250 AsnSerIleGlyArgAlaGlyArgAlaThrLeu
                                     952 TCGTTTGGCCTGGAGTCAGGCAAATGCTCTCTG
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10136
LENGTH: 2968
                                                                                                             Sequence 10136, Application US/10198846
Publication No. US20030099974A1
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US-10-198-846-10136
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387.00
58.33
37.70
29.34
                                                                                                                                     PUDLICATION CONTROL APPLICANT: Lillie, James APPLICANT: Lillie, James APPLICANT: Xu, Yongyao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
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LOCATION: 1, 2
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaAspGluIleTyrSerGluLeuLysSerMet---AlaHisIle------GlyGln 105
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    146 TyrGluLysIleLysLysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsn
                        LysLysAlaLeuLeuGlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLysLeu
                                                                               186 ArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlyIleArgLeuProPhe
                                                                                                                                               225 PheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 TyrSerLysIleValCysGluLysValGluAlaLysGlyArgThrTyrAsnGluVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 GCTTATGACCAGAAAAACATAAGACGGCGCGTCTACGATGCCTTAAACGTGCTAATGGCC
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/10206901B

Publication No. US20030100540A1

GENERAL INFORMATION:

APPLICANT: ZHANG, ZHONGHUA

TITLE OF INVENTION: IDENTIFICATION OF NSAID-REGULATED GENES

TITLE OF INVENTION: IDENTIFICATION OF NSAID-REGULATED GENES

CURRENT APPLICATION NUMBER: US/10/206,901B

CURRENT APPLICATION NUMBER: 05/308,370

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 57
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Matches:
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374.50
62.44%
41.95%
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                                                                                                                                                                                                                                                                                                                  245 GluGlyValArg 248
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SEQ ID NO 21
LENGTH: 692
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Best Local Similarity:
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Pred. No.:
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                                                                                    Sequence 43105, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Roba Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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                 300 TGACGATGTCTCAATCCTTGAAGCGATCAGGTGTAATAAT 339
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96
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63
86
 sAspAspLeuSerIleLeuGluGlyValArgArgAsnSer 251
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US-10-424-599-43105
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Mismatches:
Indels:
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Matches:
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379.50
47.89%
33.80%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                           US-10-424-599-43105
                                                                                                                                                                                                                                                                                               SEQ ID NO 43105
LENGTH: 1751
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146 TyrGluLyslleLysLysLeuGluGluValArgLysGluLeuValAsnLyslleArgAsn 165
                                                                          166 LysLysAlaLeuLeuGlnGlulleGluLysGlnPheAspAspLeuGlnAsnIleLysLeu 185
                                                                                        |||:::::: ||||||||||||:::
397 AAACAGTCTCAACTTCTACAGCAAATTGCCTTCAAGAACTGGTGCAG 456
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457 AGAAACCGGCATGCGGAGCAGCGGCCAGCCGCCACCCCAACTCAGTCATCCAC 516
                                                                                                                                                                 202 LeuProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIleSerAsp 221
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